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incl. intef!

WPPRELH (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Mon Feb 5 16:58:40 1996; MasPar time 4.63 Seconds
Tabular output not generated. 343.730 Million cell updates/sec

Title: >FIG2
Description: (1:220) from trans.pep
Perfect Score: 1643
Sequence: 1 MGAAARTIRLALGILLATL.....CAWYRGAPPKOEFIDIEP 220

Scoring table: PAM 150
Gap 11
Searched: 62355 seqs, 7230759 residues

Database: a-geneseq20
1 part1
2 part2
3 part3
4 part4
5 part5
6 part6
7 part7
8 part8
9 part9
10 part10
11 part11
12 part12

Statistics: Mean 32.075; Variance 120.092; scale 0.267
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1643	100.0	220	12	R62769 Human metalloproteinase	1.02e-170
2	1643	100.0	220	2	R07955 Human metalloproteinase	1.02e-170

3	1550	94.3	220	2	R07954	Bovine metalloproteinase	4.04e-160
4	1550	94.3	220	12	R62769	Bovine metalloproteinase	4.04e-160
5	1554	88.5	194	2	R06898	Complete sequence of	3.40e-149
6	1396	85.0	186	2	R06896	Part of TIMP-2 metallo	1.34e-142
7	1377	83.8	192	2	R06895	Metalloproteinase inh	1.93e-140
8	1337	81.4	177	2	R06897	Part of TIMP-2 metallo	6.73e-136
9	521	31.7	207	3	R60786	Sequence of tissue in	2.50e-44
10	521	31.7	207	3	R60785	Sequence of human nat	2.50e-44
11	521	31.7	207	3	R60592	Sequence of a human p	2.50e-44
12	516	31.4	207	3	R60593	Sequence of a gibbon	8.83e-44
13	323	19.7	48	2	R06749	Peptide #1 for detect	6.44e-23
14	219	13.3	28	9	R47010	Metalloproteinase inh	4.12e-12
15	170	10.3	24	2	R06894	Peptide #3 for detect	3.05e-07
16	157	9.6	19	9	R47011	Metalloproteinase inh	5.46e-06
17	149	9.1	22	2	R10001	N-terminal sequence o	3.15e-05
18	147	8.9	47	3	R60276	Immunogenic TIMP-2 pe	4.87e-05
19	140	8.5	18	2	R06747	Immunogenic TIMP-2 pe	2.21e-04
20	139	8.5	23	2	R06750	Peptide #2 for detect	2.73e-04
21	137	8.3	18	2	R10002	Tryptic digestion pro	4.19e-04
22	130	7.9	16	2	R06748	Immunogenic TIMP-2 pe	1.85e-03
23	128	7.8	15	2	R10003	Tryptic digestion pro	2.82e-03
24	118	7.2	20	6	R31183	N-terminal of monocy	2.25e-02
25	117	7.1	15	2	R06746	Immunogenic TIMP-2 pe	2.77e-02
26	116	7.1	17	8	R42187	TIMP-2 peptide P-3.	3.40e-02
27	108	6.6	18	8	R42186	TIMP-2 peptide P-2.	1.71e-01
28	104	6.3	16	8	R42185	TIMP-2 peptide P-1.	3.79e-01
29	99	6.0	3033	6	R33214	NANBH virus strain HC	1.01e+00
30	93	5.7	383	10	R36166	Neuroendocrine tumor	3.20e+00
31	91	5.5	3033	6	R33539	NANBH virus strain HC	4.67e+00
32	88	5.4	385	10	R56167	Neuroendocrine tumor	8.18e+00
33	84	5.1	389	6	R29904	HCV NS4-NS5 peptide O	1.71e+01
34	84	5.1	365	7	R38287	NANBH hepatitis virus	1.71e+01
35	82	5.0	188	9	R53358	Hyalophora cecropia a	2.45e+01
36	82	5.0	188	1	P80507	Attacin.	2.45e+01
37	82	5.0	188	9	R53347	Hyalophora cecropia a	2.45e+01
38	80	4.9	389	6	R29876	HCV NS4-NS5 O30.	3.51e+01
39	80	4.9	318	12	R64174	Adhesion protein supp	3.51e+01
40	80	4.9	730	1	P80618	Human Bone Morphogeni	3.51e+01
41	79	4.8	389	6	R29905	HCV NS4-NS5 peptide O	4.19e+01
42	79	4.8	1411	6	R29533	HCV NS4-NS5 peptide I	4.19e+01
43	79	4.8	389	6	R29906	HCV NS4-NS5 peptide O	4.19e+01
44	79	4.8	1013	12	R62535	P. vulgaris chondroit	4.19e+01
45	79	4.8	323	1	R05711	Tumour-associated ant	4.19e+01

ALIGNMENTS

RESULT 1
ID R62769 standard; Protein; 220 AA.
AC R62769;
DT 13-JUL-1995 (first entry)
DE Human metalloproteinase inhibitor.
KW Metalloproteinase inhibitor; tumour cell dissemination;
KW rheumatoid arthritis; cystrophic epidermolysis bullosa;
OS emphysema; osteoporosis; MI gene disorders.
KW Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..26
FT /label= sig_peptide
PN EP-623676-A.

PD 09-NOV-1994.
 PF 18-MAY-1990; 305433.
 PR 19-MAY-1989; US-355027.
 PR 29-MAR-1990; US-501904.
 PA (AMGE-) AMGEN INC.
 PA (CHIL-) CHILDREN'S HOSPITAL LOS ANGELES.
 PI Boone TC, Declerck YA, Langley KE;
 DR WPI; 94-343309/43.
 DR N-PSDB; Q73088.
 PT New metalloproteinase inhibitor, analogues and DNA - for
 PT treating tumour cell dissemination, rheumatoid arthritis and for
 PT large-scale recombinant inhibitor prodn.
 PS Claim 8; Fig 2; 63pp; English.
 CC Q73088 encodes R62769 human metalloproteinase inhibitor (MI), it
 CC may be used to inhibit tumour cell dissemination and for treating
 CC rheumatoid arthritis, dystrophic epidermolysis bullosa, emphysema
 CC and osteoporosis. The DNA may be used to detect MI gene disorders.
 SQ Sequence 220 AA;
 DB 12; Score 1643; Match 100.0%; QryMatch 100.0%; Pred. No. 1.02e-170;
 Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 mgaartlralqllllatllrpacscspvhpqgafcnadvirakavsekevdsgnd 60
 Qy 1 MGAARTLRLALGILLLLATLLRPADACSCSPVHPQQAFCNADVIRAKAVSEKEVDSGND 60
 Db 61 iynpikriqveikqikmfkgpekdiefiytapssavcgvslvvggkkeyliagkaegdg 120
 Qy 61 IYGNPIKRIQVEIKQIKMFKGPEKDEFIYTAPSSAVCGVSLVVGKKEYLIAGKAEGDG 120
 Db 121 kmhitlcdfvpwdtltstqkkslnhrygmgeckitrcpmipcyisspdeclmwdwvte 180
 Qy 121 KMHTLCDVFVPWDTLTSTQKKS LNHR YQMGECKITRCPMIPCYISSPDECLMWDWVTE 180
 Db 181 kninghqakffacikrdsdscawyrqgappkqefldiedp 220
 Qy 181 KNINGHQAKFFACIKRSDGSCAWYRGAPPKQEFLDIEDP 220
 RESULT 2
 ID R07955 standard; protein; 220 AA.
 AC R07955;
 DT 21-FEB-1991 (first entry)
 DE Human metalloproteinase inhibitor gene product.
 KW Tumour; chemotherapy; cancer; Paget's disease; osteoporosis;
 KW scleroderma; cholesteatoma.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Protein 27..220
 PN EP-398753-A.
 PD 22-NOV-1990.
 PF 18-MAY-1990; 305433.
 PR 19-MAY-1989; US-355027.
 PR 29-MAR-1990; US-501904.
 PA (AMGE-) AMGEN INC.
 PA (CHIL-) CHILDREN'S HOSPITAL OF LA.
 PI Langley KE, Boone TC, Declerck YA;
 DR WPI; 90-350481/47.
 DR N-PSDB; Q06584.
 PT New metalloproteinase inhibitor polypeptide(s) - and DNA

PT encoding them, for treatment of tumour cell dissemination and
 PT rheumatoid arthritis
 PS Claim 12; Fig 2; 63pp; English.
 CC The product has therapeutic use in inhibiting tumour dissemination
 CC during chemotherapy and radiation therapy, impurged bone marrow cell
 CC harvesting etc. The inhibitor may also be useful in encapsulating
 CC tumours aiding clean excision, and in treatment of emphysema, Paget's
 CC disease, osteoporosis, scleroderma and bedsores.
 CC The gene product also has application in autoimmune disorders eg.
 CC rheumatoid arthritis and multiple sclerosis.
 CC See also Q06583.
 SQ Sequence 220 AA;
 DB 2; Score 1643; Match 100.0%; QryMatch 100.0%; Pred. No. 1.02e-170;
 Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 mgaartlralqllllatllrpacscspvhpqgafcnadvirakavsekevdsgnd 60
 Qy 1 MGAARTLRLALGILLLLATLLRPADACSCSPVHPQQAFCNADVIRAKAVSEKEVDSGND 60
 Db 61 iynpikriqveikqikmfkgpekdiefiytapssavcgvslvvggkkeyliagkaegdg 120
 Qy 61 IYGNPIKRIQVEIKQIKMFKGPEKDEFIYTAPSSAVCGVSLVVGKKEYLIAGKAEGDG 120
 Db 121 kmhitlcdfvpwdtltstqkkslnhrygmgeckitrcpmipcyisspdeclmwdwvte 180
 Qy 121 KMHTLCDVFVPWDTLTSTQKKS LNHR YQMGECKITRCPMIPCYISSPDECLMWDWVTE 180
 Db 181 kninghqakffacikrdsdscawyrqgappkqefldiedp 220
 Qy 181 KNINGHQAKFFACIKRSDGSCAWYRGAPPKQEFLDIEDP 220
 RESULT 3
 ID R07954 standard; protein; 220 AA.
 AC R07954;
 DT 21-FEB-1991 (first entry)
 DE Bovine metalloproteinase inhibitor gene product.
 KW Tumour; chemotherapy; cancer; Paget's disease; osteoporosis;
 KW scleroderma; cholesteatoma.
 OS Bos taurus.
 FH Key Location/Qualifiers
 FT Protein 27..220
 PN EP-398753-A.
 PD 22-NOV-1990.
 PF 18-MAY-1990; 305433.
 PR 19-MAY-1989; US-355027.
 PR 29-MAR-1990; US-501904.
 PA (AMGE-) AMGEN INC.
 PA (CHIL-) CHILDREN'S HOSPITAL OF LA.
 PI Langley KE, Boone TC, Declerck YA;
 DR WPI; 90-350481/47.
 DR N-PSDB; Q06583.
 PT New metalloproteinase inhibitor polypeptide(s) - and DNA
 PT encoding them, for treatment of tumour cell dissemination and
 PT rheumatoid arthritis
 PS Claim 12; Fig 1; 63pp; English.
 CC The product has therapeutic use in inhibiting tumour dissemination
 CC during chemotherapy and radiation therapy, impurged bone marrow cell
 CC harvesting etc. The inhibitor may also be useful in encapsulating

CC tumours aiding clean excision, and in treatment of enphysema, Paget's disease, osteoporosis, scleroderma and bedsores.
 CC The gene product also has application in autoimmune disorders eg. rheumatoid arthritis and multiple sclerosis.
 CC See also Q06584.
 SQ Sequence 220 AA;

DB 2; Score 1550; Match 91.8%; QryMatch 94.3%; Pred. No. 4.04e-160;
 Matches 202; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

Db 1 mgaarslplafcllllgtllpradacscspvhpqafcnadivirakavnkkevsgnd 60
 Qy 1 MGAARTLRALGELLATLLRPADACSCSPVHPQQAFCNADVIRAKAVSEKVEVSGND 60

Db 61 iynpnkriqyeikqimfkpgdqdiefiytapaavcgsvldvgkkeyliagkaegng 120
 Qy 61 IYGNPIKRIQYEIKQIMFKGPEKDIEFIYTAPSAVCGSVLDVGKKEYLIAGKAEGDG 120

Db 121 nmhtlcldfivpwtltsatqkkslnhrygmgeckitrcpmipcyisspdeclmwdvte 180
 Qy 121 KMHITLCLDFIVPWTLTSTQKSLNHRVQMGCECKITRCMPICYSISPDECLMWDWTE 180

Db 181 kninghqakffacikrdsqscawyrqgaappkqefldiedp 220
 Qy 181 KNINGHQAKFFACIKRDSQSCAWYRGAPPKQEFLDIEDP 220

RESULT 4
 ID R62768 standard; Protein; 220 AA.
 AC R62768;
 DT 13-JUL-1995 (first entry)
 DE Bovine metalloproteinase inhibitor
 KW Metalloproteinase inhibitor; tumour cell dissemination;
 KW rheumatoid arthritis; dystrophic epidermolysis bullosa;
 KW emphysema; osteoporosis; MI gene disorders.
 OS Bos taurus.
 FH Key Location/Qualifiers
 FT Peptide 1..26
 FT /label= sig peptide
 PN EP-623676-A.
 PD 09-NOV-1994.
 PF 18-MAY-1990; 305433.
 PR 19-MAY-1989; US-355027.
 PR 29-MAR-1990; US-501904.
 PA (AMGE-) AMGEN INC.
 PA (CHIL-) CHILDRENS HOSPITAL LOS ANGELES.
 PI Boone TC, Declerck YA, Langley KE;
 DR WPI; 94-34309/43.
 DR N-PSDB; Q73087.
 PT New metalloproteinase inhibitor, analogues and DNA - for treating tumour cell dissemination, rheumatoid arthritis and for large-scale recombinant inhibitor prodn.
 PS Claim 12; Fig 1; 65pp; English.
 CC Q73087 encodes R62768 bovine metalloproteinase inhibitor (MI), it may be used to inhibit tumour cell dissemination and for treating rheumatoid arthritis, dystrophic epidermolysis bullosa, emphysema and osteoporosis. The DNA may be used to detect MI gene disorders.
 SQ Sequence 220 AA;

DB 12; Score 1550; Match 91.8%; QryMatch 94.3%; Pred. No. 4.04e-160;

Matches 202; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

Db 1 mgaarslplafcllllgtllpradacscspvhpqafcnadivirakavnkkevsgnd 60
 Qy 1 MGAARTLRALGELLATLLRPADACSCSPVHPQQAFCNADVIRAKAVSEKVEVSGND 60

Db 61 iynpnkriqyeikqimfkpgdqdiefiytapaavcgsvldvgkkeyliagkaegng 120
 Qy 61 IYGNPIKRIQYEIKQIMFKGPEKDIEFIYTAPSAVCGSVLDVGKKEYLIAGKAEGDG 120

Db 121 nmhtlcldfivpwtltsatqkkslnhrygmgeckitrcpmipcyisspdeclmwdvte 180
 Qy 121 KMHITLCLDFIVPWTLTSTQKSLNHRVQMGCECKITRCMPICYSISPDECLMWDWTE 180

Db 181 kninghqakffacikrdsqscawyrqgaappkqefldiedp 220
 Qy 181 KNINGHQAKFFACIKRDSQSCAWYRGAPPKQEFLDIEDP 220

RESULT 5
 ID R06898 standard; protein; 194 AA.
 AC R06898;
 DT 16-JAN-1991 (first entry)
 DE Complete sequence of human TIMP-2 from clone pSS38.
 KW matrix metalloproteinase inhibitor; TIMP-2; pSS38.
 OS Synthetic.
 PN US7494796-A.
 PD 21-AUG-1990.
 PF 13-MAR-1990; 494796.
 PR 17-MAR-1989; US-326334.
 PR 21-JUL-1989; US-380431.
 PR 18-AUG-1989; US-395453.
 PR 13-MAR-1990; US-494796.
 PA (USSH) NAT INST OF HEALTH.
 PI Stetler-Sevenson WG, Liotta LA, Krutzsch HC;
 DR WPI; 90-290097/38.
 DR N-PSDB; Q05940.
 PT New matrix metallo-proteinase inhibitor - used to treat diseases resulting from matrix metallo-proteinase activity and in diagnosis, detection and purification.
 PS Disclosure; Fig 7; 54pp; English.
 CC TIMP-2 was isolated from human melanoma cell-conditioned media and the amino acid sequence determined. A probe was synthesised based upon the protein sequence information. It was used to screen a LambdaGem-4 cDNA library prepared from human melanoma cells. 239 positives were identified from a total of 750,000 plaques screened. Further analysis and screening with additional probes eliminated most of the clones. Clone pSS38 was isolated and the nucleotide sequence of the cDNA insert was determined. The deduced amino acid sequence showed excellent agreement with that derived by directly sequencing the TIMP-2 protein.
 CC See also Q05937, R06746-R06750, R06894-R06895 and Q05938-Q05939.
 SQ Sequence 194 AA;

DB 2; Score 1454; Match 99.5%; QryMatch 88.5%; Pred. No. 3.40e-149;
 Matches 193; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 cscapvhpqafcnadivirakavsekdsgndiynpnkriqyeikqimfkqgpekdi 60
 Qy 27 CSCSPVHPQQAFCNADVIRAKAVSEKVEVSGNDIYNPNKRIQYEIKQIMFKGPEKDI 86

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Db 61 eflytapsavcgvslvvgkkeyliagkaedgkmhltcdflvpwdtltsttkkslnh 120
QY 87 EFYITAPSAVCGVSLVVGKKEYLIAGKAEDGKMHITLGDFlVPWDTLTSTTKKSLNH 146
Db 121 rymgceckitrcpmipcyisspdeclwmwvteknngqakffacikrsdgcawyr 180
QY 147 RYMGCECKITRCPMIPCYISSPDECLWMWVTEKNNGHQAKFFACIKRSDGSCAWYRG 206
Db 181 aappkqefldiedp 194
QY 207 AAPPKQEFLDIEDP 220

RESULT 6
ID R06896 standard; protein; 186 AA.
AC R06896;
DT 16-JAN-1991 (first entry)
DE Part of TIMP-2 metalloproteinase inhibitor, encoded by clone pSS15.
KW matrix metalloproteinase inhibitor; TIMP-2; pSS15.
OS Synthetic.
PN US7494796-A.
PD 21-AUG-1990.
PF 13-MAR-1990; 494796.
PR 21-MAR-1989; US-326334.
PR 17-JUL-1989; US-380431.
PR 18-AUG-1989; US-395453.
PR 13-MAR-1990; US-494796.
PA (USSH ) NAT INST OF HEALTH.
PI Stetler-Sevenson WG, Liotta LA, Krutzsch HC;
DR N-PSDB; Q05938.
DR R06896;
PT New matrix metallo-proteinase inhibitor - used to treat diseases
PT resulting from matrix metallo-proteinase activity and in
PT diagnosis, detection and purificn..
PS Disclosure; Fig 8A; 54pp; English.
CC TIMP-2 was isolated from human melanoma cell-conditioned media and
CC the amino acid sequence determined. A probe was synthesised
CC based upon the protein sequence information. It was used to screen
CC a LambdaGen-4 cDNA library prepared from human melanoma cells. 239
CC positives were identified from a total of 750,000 plaques screened.
CC Further analysis and screening with additional probes eliminated
CC all but two clones (pSS15 and pSS18). Both were sequenced and found
CC to encode CSC-21K (=TIMP-2), a novel metalloproteinase inhibitor.
CC This is the amino acid sequence deduced from the cDNA sequence of
CC pSS15.
CC See also Q05937, R06746-R06750, R06894-R06895 and Q05939-Q05940.
SQ Sequence 186 AA;

DB 2; Score 1396; Match 99.5%; QryMatch 85.0%; Pred. No. 1.34e-142;
Matches 185; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 1 qqafcnadvirakavnskevdsngndiynpikriqyeikqkfkgekieftaps 60
QY 35 QQAFCNADVIRAKAVNSKEVDSNGNDIYNPIKRIQYEIKQKFKGFKGKIEFTAPS 94
Db 61 savcgvslvvgkkeyliagkaedgkmhltcdflvpwdtltsttkkslnhrymgcec 120
QY 95 SAVCGVSLVVGKKEYLIAGKAEDGKMHITLGDFlVPWDTLTSTTKKSLNHRYMGCCEC 154

Db 121 kitrcpmipcyisspdeclwmwvteknngqakffacikrsdgcawyr 180
QY 155 KITRCPMIPCYISSPDECLWMWVTEKNNGHQAKFFACIKRSDGSCAWYRGAPPKQEF 214
Db 181 ldiedp 186
QY 215 LDIEDP 220

RESULT 7
ID R06895 standard; protein; 192 AA.
AC R06895;
DT 16-JAN-1991 (first entry)
DE Metalloproteinase inhibitor TIMP-2.
KW matrix metalloproteinase inhibitor; TIMP-2 (CSC-21K).
OS Synthetic.
PN US7494796-A.
PD 21-AUG-1990.
PF 13-MAR-1990; 494796.
PR 21-MAR-1989; US-326334.
PR 17-JUL-1989; US-380431.
PR 18-AUG-1989; US-395453.
PR 13-MAR-1990; US-494796.
PA (USSH ) NAT INST OF HEALTH.
PI Stetler-Sevenson WG, Liotta LA, Krutzsch HC;
DR WPI; 90-290097/38.
DR R06895;
PT New matrix metallo-proteinase inhibitor - used to treat diseases
PT resulting from matrix metallo-proteinase activity and in
PT diagnosis, detection and purificn..
PS Disclosure; Fig 5; 54pp; English.
CC Protein was isolated from human melanoma cell-conditioned media by
CC gelatin-affinity chromatography.
CC It inhibits matrix metalloproteinases and can be used to treat
CC diseases such as arthritis, diabetes, cancer, ulcers of mucosa and
CC epithelial tissues, autoimmune-mediated inflammation, lung injury,
CC granulomatous diseases and myocardial infarctions. It can also be
CC used as a birth control agent by preventing embryoplacental
CC attachment or invasion. Other therapeutic benefits may also be
CC obtd. in diseases with basement destruction or myocyte destruction.
CC See also Q05937, R06746-R06750, R06894 and Q05938-Q05940.
SQ Sequence 192 AA;

DB 2; Score 1377; Match 96.4%; QryMatch 83.8%; Pred. No. 1.93e-140;
Matches 186; Conservative 1; Mismatches 5; Indels 1; Gaps 1;
Db 1 cscapvhpgafcnadvirakavnskevdsngndiynpikriqyeikqkfkgekiekdi 60
QY 27 CSCAPVHPGQAFCNADVIRAKAVNSKEVDSNGNDIYNPIKRIQYEIKQKFKGFKEDI 86
Db 61 eflytapsavcgvslvvgkkeyliagkaedgkmhltcdflvpwdtltsttkkslnh 119
QY 87 EFYITAPSAVCGVSLVVGKKEYLIAGKAEDGKMHITLGDFlVPWDTLTSTTKKSLNH 146
Db 120 rymgceckitrcpmipcyisspdeclwmwvteknngqakffacikrsdgcawyr 179
QY 147 RYMGCECKITRCPMIPCYISSPDECLWMWVTEKNNGHQAKFFACIKRSDGSCAWYRG 206
Db 180 aappkqefldied 192
QY 207 AAPPKQEFLDIED 219
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FH	Key	Location/Qualifiers
FT	Peptide	1..23
FT	/label= signal	
FT	Protein	53..207
FT	Modified -site	24..55
FT	/label= potential N-glycosylation site	
FT	Modified -site	101..103
FT	/label= as above	
PN	GS2169295-A.	
PN	09-JUL-1986.	
PF	05-JAN-1986;	000199.
PF	05-OCT-1983;	BE-897924.
PR	07-JAN-1985;	GB-000341.
PR	07-JAN-1985;	GB-500341.
PR	01-NOV-1985;	GB-026951.
PR	06-JAN-1986;	GB-000199.
PA	(CELL-) CELTECH LTD.	
PI	Harris TJR, Reynolds JJ, Docherty AJP,	
DR	WFI; 86-177873/28.	
DR	N-PSDB; N60538.	
PT	Prodn. of metallo-proteinase inhibitor techniques	
PT	Disclosure; Fig 3; 16pp; English.	
PS	A gene with residues 64-684 of N60538	
CC	Isolated from human a foetal diploid library using N60539.	
SC	Sequence	207 AA;
DB	3; Score	521; Match 41.1%; Qryv
	Matches	81; Conservative 39; Mismat
Db	7 laaglllllwliaapractcvpphqtafcnsg	
Qy	10 LALGLLGLLTLATLRPADACSCSPVHPQQAFCNADY	
Db	66 tk-mykqfcal-gdaadirfvytpamesvcvyfll	
Qy	69 IQYEIKQIKMFKGPKEDIEFYTPAPSSAVCGVS	
Db	123 sfvapwnslsagrqtktvtvcgeetvfpc	
Qy	128 DFIVPMDTLSTOKSLNHRVQMGE-CKITRCL	
Db	183 qsrhlacilpreplgtw 199	
Qy	187 QAKFFACIKRSDGSCAW 203	
RESULT	10	
ID	P60275 standard; Protein; 207 AA.	
AC	P60275;	
DT	08-AUG-1991 (first entry)	
DE	Sequence of human natural inhibitor of	
KW	Metallo-proteinase inhibitor; wound he	
KW	rheumatoid arthritis therapy; ulcerati	
FH	Key	Location/Qualifiers
FT	Peptide	1..23
FT	/label= signal	
FT	Protein	24..207
FT	/note= "claimed"	

Key	Location/Qualifiers
FT Peptide	1..23
FT /label= signal	
FT Protein	24..207
FT /note= "claimed"	

[illegible]

Db 7 lasgilllllwlapiactcvphqqtatfensdlvikakfvgtpevnqgt-lyqrveikm 65
 Qy 10 LAIGLLLLAVLLRPADACSCSPVHPQQAFCNADVVIRAKAVSEKVDSDNDIYGN-PIKR 68
 Db 66 tk-mykgfql-gdaadirfvytpamesvcgyfhrshnrseefliagklq-dgllhittc 122
 Qy 69 IQYEIKQIKMFKGPEKDIEFIYAPSSAVCGVSLDVGKKE-YLIAGRAEGDKMHTLC 127
 Db 123 sfvapwnslagrrgtfkytvgceectvfpclsipklqsgthclwtldllgsekqf 182
 Qy 128 DFIVPMDTLTQKSLNHYQMGCE-CRITRCPMIPCVISSPDECLWMDWVTEKNIGH 186
 Db 183 qsrhlacipreglctw 199
 Qy 187 QAKFFACIKRSDGSCAW 203

RESULT 13
 ID R06749 standard; protein; 48 AA.
 AC R06749;
 DT 16-JAN-1991 (first entry)
 DE Peptide #1 for detection of metalloproteinases.
 KW matrix metalloproteinase; TIMP-2 (CSC-21K).
 OS Synthetic.
 PN US7494796-A.
 PD 21-AUG-1990.
 PF 13-MAR-1990; 494796.
 PR 21-MAR-1989; US-326334.
 PR 17-JUL-1989; US-380431.
 PR 18-AUG-1989; US-395453.
 PR 13-MAR-1990; US-494796.
 PA (USSH) NAT INST OF HEALTH.
 PI Stetler-Sevenson WG, Liotta LA, Krutzsch HC;
 DR WPI; 90-290097/38.
 PT New matrix metallo-proteinase inhibitor - used to treat diseases
 PT resulting from matrix metallo-proteinase activity and in
 PT diagnosis, detection and purificn..
 PS Example; Page 37; 54pp; English.
 CC One of three peptides lacking cysteine or having only one cysteine
 CC which were found to be useful for detecting metalloproteinases in
 CC animal and human tissues or in body fluids which may have
 CC antibodies to the protein. The peptides can also be used to elicit
 CC antibodies for use in detecting metalloproteinases.
 CC See also Q05937, R06746-R06748, R06750, R06894-R06895 and
 CC Q05938-Q05940.
 SQ Sequence 48 AA;

DB 2; Score 323; Match 93.8%; QryMatch 19.7%; Pred. No. 6.44e-23;
 Matches 45; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 1 diygnpikriqyeikgikfkgtiekdiefiytpassavcgveldvggk 48
 Qy 60 DIVGNPIKRIQYIKQIKMFKGPEKDIEFIYTPASSAVCGVSLDVGGK 107

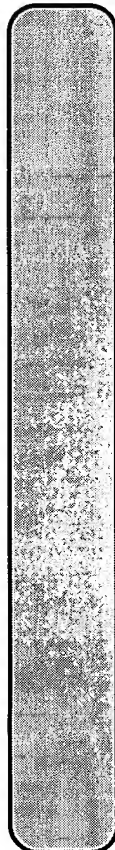
RESULT 14
 ID R47010 standard; Protein; 28 AA.
 AC R47010;
 DT 16-SEP-1994 (first entry)
 DE Metalloproteinase inhibitor 2 position 187-214.

KW Naturally-occurring; immunomodulatory protein; human; therapy; class I;
 KW major histocompatibility complex; class II; allotype; type I diabetes;
 KW autoimmune disease; rheumatoid arthritis; T-cell-mediated response;
 KW multiple sclerosis; transplant rejection; vaccine; MHC.
 OS Homo sapiens.
 PN WO9404171-A.
 PD 03-MAR-1994.
 PF 11-AUG-1993; U07545.
 PR 11-AUG-1992; US-925460.
 PR 15-JUN-1993; US-925460.
 PA (HARD) HARVARD COLLEGE.
 PI Chicz RM, Hedley ML, Stern LJ, Strominger JL, Urban RG;
 PI Vignali DA;
 DR WPI; 94-082825/10.
 PT Novel immunomodulatory peptide(s) and nucleic acids - useful for
 PT treatment of auto-immune diseases, transplant rejection and for
 PT vaccination
 PS Disclosure; Page 48; 139pp; English.
 CC The sequences given in R43291-505 and R46981-7038 represent peptide
 CC fragments of naturally-occurring immunomodulatory proteins. These
 CC fragments are between 10-30 residues in length and bind to a human
 CC major histocompatibility complex (MHC) class II allotype. These
 CC peptides may be used for therapy of autoimmune diseases, such as
 CC type I diabetes, rheumatoid arthritis and multiple sclerosis, and to
 CC reduce transplant rejection. They may also be used for vaccination
 CC providing an exclusively T-cell-mediated response, which can be
 CC class I or class-II based, or both, depending on the length and
 CC character of the immunogenic peptides.
 SQ Sequence 28 AA;

DB 9; Score 219; Match 100.0%; QryMatch 13.3%; Pred. No. 4.12e-12;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 qakffacikrsgdscawyrqaaapkpqef 28
 Qy 187 QAKFFACIKRSDGSCAWYRGAAAPKQEF 214

RESULT 15
 ID R06894 standard; protein; 24 AA.
 AC R06894;
 DT 16-JAN-1991 (first entry)
 DE Peptide #3 for detection of metalloproteinases.
 KW matrix metalloproteinase; TIMP-2 (CSC-21K).
 OS Synthetic.
 PN US7494796-A.
 PD 21-AUG-1990.
 PF 13-MAR-1990; 494796.
 PR 21-MAR-1989; US-326334.
 PR 17-JUL-1989; US-380431.
 PR 18-AUG-1989; US-395453.
 PR 13-MAR-1990; US-494796.
 PA (USSH) NAT INST OF HEALTH..
 PI Stetler-Sevenson WG, Liotta LA, Krutzsch HC;
 DR WPI; 90-290097/38.
 PT New matrix metallo-proteinase inhibitor - used to treat diseases
 PT resulting from matrix metallo-proteinase activity and in
 PT diagnosis, detection and purificn..
 PS Example; Page 37; 54pp; English.
 CC One of three peptides lacking cysteine or having only one cysteine



CC which were found to be useful for detecting metalloproteinases in
 CC animal and human tissues or in body fluids which may have
 CC antibodies to the protein. The peptides can also be used to elicit
 CC antibodies for use in detecting metalloproteinases.
 CC See also Q05937, R06746-R06750, R06895 and Q05938-Q05940.
 SQ Sequence 24 AA;

DB 2; Score 170; Match 100.0%; QryMatch 10.3%; Pred. No. 3.05e-07;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 hitcdflvpwdltsttkksln 24
 QY 123 HITLDFIVPWTLSITTKKSLN 145

Search completed: Mon Feb 5 16:59:06 1996
 Job time : 26 secs.

W P S R L H (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Mon Feb 5 17:01:32 1996; MasPar time 2.09 Seconds
 Tabular output not generated.
 194.539 Million cell updates/sec

Title: >FIG2
 Description: (1:220) from trans.pep
 Perfect Score: 1643
 Sequence: 1 MGAARTLRALGLLLATL.....CAWYRGAPPKOEFIDIEDP 220

Scoring table: PAM 150
 Gap 11

Searched: 19663 seqs, 1851369 residues

Database: a-issued
 1 51
 2 52
 3 53
 4 54
 5 PCT90
 6 PCT91
 7 PCT92
 8 PCT93
 9 PCT94
 10 PCT95

Statistics: Mean 30.075; Variance 124.991; scale 0.241

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description	Pred. No.
1	219	13.3	28	8	PCT-US93-0 Sequence 245, Applicat	1.40e-11
2	157	9.6	19	8	PCT-US93-0 Sequence 246, Applicat	5.57e-06
3	91	5.5	3033	4	US-07-925- Sequence 9, Applicatio	1.68e+00
4	91	5.5	3033	4	US-07-925- Sequence 8, Applicatio	1.68e+00
5	79	4.8	990	10	PCT-US95-0 Sequence 2, Applicatio	1.32e+01
6	79	4.8	476	9	PCT-US94-0 Sequence 12, Applicati	1.32e+01
7	79	4.8	397	10	PCT-US95-0 Sequence 14, Applicati	1.32e+01
8	75	4.6	928	9	PCT-US94-1 Sequence 3, Applicatio	2.55e+01
9	75	4.6	928	9	PCT-US94-1 Sequence 13, Applicatio	2.55e+01
10	74	4.5	490	10	PCT-US95-0 Sequence 4, Applicatio	3.00e+01
11	74	4.5	778	8	PCT-US93-0 Sequence 2, Applicatio	3.00e+01
12	74	4.5	480	4	US-07-803- Sequence 2, Applicatio	3.00e+01
13	73	4.4	883	3	US-08-106- Sequence 2, Applicatio	3.53e+01
14	71	4.3	659	10	PCT-US95-0 Sequence 8, Applicatio	4.86e+01
15	70	4.3	239	8	PCT-US93-0 Sequence 1, Applicatio	5.70e+01
16	70	4.3	2446	8	PCT-US93-0 Sequence 2, Applicatio	5.70e+01
17	70	4.3	1513	8	PCT-US93-0 Sequence 3, Applicatio	5.70e+01
18	70	4.3	778	8	PCT-US93-0 Sequence 3, Applicatio	5.70e+01
19	70	4.3	112	8	PCT-US93-0 Sequence 3, Applicatio	5.70e+01
20	69	4.2	104	3	US-07-789- Sequence 8, Applicatio	6.67e+01
21	69	4.2	180	4	US-07-953- Sequence 12, Applicatio	6.67e+01
22	69	4.2	286	8	PCT-US93-0 Sequence 65, Applicati	6.67e+01
23	69	4.2	336	7	PCT-US92-1 Sequence 2, Applicatio	6.67e+01
24	68	4.1	474	10	PCT-US95-0 Sequence 5, Applicatio	7.80e+01
25	68	4.1	434	2	US-07-679- Sequence 15, Applicati	7.80e+01
26	68	4.1	567	4	US-08-007- Sequence 2, Applicatio	7.80e+01
27	68	4.1	214	4	US-07-953- Sequence 11, Applicati	7.80e+01
28	68	4.1	575	3	US-07-683- Sequence 2, Applicatio	7.80e+01
29	67	4.1	3011	9	PCT-US94-0 Sequence 1, Applicatio	9.12e+01
30	67	4.1	3011	10	PCT-US95-0 Sequence 1, Applicatio	9.12e+01
31	67	4.1	364	8	PCT-US93-1 Sequence 5, Applicatio	9.12e+01
32	67	4.1	3033	4	US-07-925- Sequence 1, Applicatio	9.12e+01
33	67	4.1	3011	8	PCT-US93-0 Sequence 4, Applicatio	9.12e+01
34	67	4.1	69	4	US-08-175- Sequence 3, Applicatio	9.12e+01
35	67	4.1	355	6	PCT-US91-0 Sequence 2, Applicatio	9.12e+01
36	67	4.1	782	4	US-07-725- Sequence 2, Applicatio	9.12e+01
37	67	4.1	364	8	PCT-US93-1 Sequence 15, Applicati	9.12e+01
38	66	4.0	21	2	US-07-679- Sequence 9, Applicatio	1.06e+02
39	66	4.0	477	3	US-07-847- Sequence 2, Applicatio	1.06e+02
40	66	4.0	481	9	US-08-186- Sequence 2, Applicatio	1.06e+02
41	66	4.0	481	9	PCT-US94-0 Sequence 4, Applicatio	1.06e+02
42	66	4.0	1167	3	US-08-100- Sequence 2, Applicatio	1.06e+02
43	66	4.0	18	10	PCT-US95-0 Sequence 187, Applicati	1.06e+02
44	66	4.0	29	9	PCT-US94-0 Sequence 30, Applicati	1.06e+02
45	66	4.0	481	10	PCT-US95-0 Sequence 98, Applicati	1.06e+02

ALIGNMENTS

Listing for Mary Hale Tue Feb 6 11:36:52 1996

RESULT 1
ID PCT-US93-07545-245 STANDARD; PRT; 28 AA.
XX -
AC xxxxxx
DT 01-JAN-1900
XX Sequence 245, Application PC/TUS9307545.
DE Sequence 245, Application PC/TUS9307545.
XX GENERAL INFORMATION:
CC APPLICANT: Robert G. Urban
CC APPLICANT: Roman M. Chicz
CC APPLICANT: Dario A. A. Vignali
CC APPLICANT: Mary L. Hedley
CC APPLICANT: Lawrence J. Stern
CC APPLICANT: Jack L. Strominger
CC TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
CC NUMBER OF SEQUENCES: 273
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Fish & Richardson
CC STREET: 225 Franklin Street
CC CITY: Boston
CC STATE: Massachusetts
CC COUNTRY: U.S.A.
CC ZIP: 02110-2804
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
CC COMPUTER: IBM PS/2 Model 502 or 55SX
CC OPERATING SYSTEM: MS-DOS (Version 5.0)
CC SOFTWARE: WordPerfect (Version 5.1)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US93/07545
CC FILING DATE: 19930811
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/925,460
CC FILING DATE: August 11, 1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Clark, Paul T.
CC REGISTRATION NUMBER: 30,162
CC REFERENCE/DOCKET NUMBER: 00246/168001
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (617) 542-5070
CC TELEFAX: (617) 542-8906
CC TELEX: 200154
CC INFORMATION FOR SEQ ID NO: 245:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 28
CC TYPE: amino acid
CC STRANDEDNESS:
CC TOPOLOGY: linear
CC SEQUENCE 28 AA; 3164 MW; 3693 CN;
DB 8; Score 219; Match 100.0%; QryMatch 13.3%; Pred. No. 1.40e-11;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 OAKFFACIKRSDGSCAWYGAAPPKQEF 28
|||||

Listing for Mary Hale Tue Feb 6 11:36:52 1996

OY 187 OAKFFACIKRSDGSCAWYGAAPPKQEF 214
RESULT 2
ID PCT-US93-07545-246 STANDARD; PRT; 19 AA.
XX -
AC xxxxxx
DT 01-JAN-1900
XX Sequence 246, Application PC/TUS9307545.
DE Sequence 246, Application PC/TUS9307545.
XX GENERAL INFORMATION:
CC APPLICANT: Robert G. Urban
CC APPLICANT: Roman M. Chicz
CC APPLICANT: Dario A. A. Vignali
CC APPLICANT: Mary L. Hedley
CC APPLICANT: Lawrence J. Stern
CC APPLICANT: Jack L. Strominger
CC TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
CC NUMBER OF SEQUENCES: 273
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Fish & Richardson
CC STREET: 225 Franklin Street
CC CITY: Boston
CC STATE: Massachusetts
CC COUNTRY: U.S.A.
CC ZIP: 02110-2804
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
CC COMPUTER: IBM PS/2 Model 502 or 55SX
CC OPERATING SYSTEM: MS-DOS (Version 5.0)
CC SOFTWARE: WordPerfect (Version 5.1)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US93/07545
CC FILING DATE: 19930811
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/925,460
CC FILING DATE: August 11, 1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Clark, Paul T.
CC REGISTRATION NUMBER: 30,162
CC REFERENCE/DOCKET NUMBER: 00246/168001
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (617) 542-5070
CC TELEFAX: (617) 542-8906
CC TELEX: 200154
CC INFORMATION FOR SEQ ID NO: 246:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 19
CC TYPE: amino acid
CC STRANDEDNESS:
CC TOPOLOGY: linear
CC SEQUENCE 19 AA; 2238 MW; 1748 CN;
DB 8; Score 157; Match 100.0%; QryMatch 9.6%; Pred. No. 5.57e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC TELEEX: WUI 64470
CC INFORMATION FOR SEQ ID NO: 8:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 3033 amino acids
CC TYPE: AMINO ACID
CC STRANDEDNESS: unknown
CC TOPOLOGY: linear
CC SEQUENCE 3033 AA; 330178 MW; 48732738 CN;

DB 4; Score 91; Match 25.5%; QryMatch 5.5%; Pred. No. 1.68e+00;
Matches 24; Conservative 27; Mismatches 37; Indels 6; Gaps 5;

Db 2739 IKALACKAAGIVDPVMLVCGDDIAVISESQNEEDERNLRAFTEAMTR--YSAPPGDLP 2796
QY 21 LRADACSCSP-VHPQAFNCADVIRAKAVSEKVDSGNDIYGNPIKRIQFIKQIKMF 79

Db 2797 R-PEYDLELI-TSCSNV-SVALDSRGRRRYFLT 2827
QY 80 KGPEKDIEFIYAPSSAVCGVSLDVGGKKEYLIA 113

RESULT 5
ID PCT-US95-04656-2 STANDARD; PRT; 990 AA.
XX AC xxxxxx
XX 01-JAN-1900
DE Sequence 2, Application PC/TUS9504656.
XX Sequence 2, Application PC/TUS9504656
CC GENERAL INFORMATION:
CC APPLICANT: Khandke, Kiran M.
CC TITLE OF INVENTION: A Novel Protein Designated
CC TITLE OF INVENTION: Chondroitinase II and its Use With a Protein Desi
CC gnated
CC TITLE OF INVENTION: Chondroitinase I to Achieve Complete Vitreal Disi
CC nsertion
CC NUMBER OF SEQUENCES: 2
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: American Cyanamid Company
CC STREET: One Cyanamid Plaza
CC CITY: Wayne
CC STATE: New Jersey
CC COUNTRY: U.S.A.
CC ZIP: 07470-8426
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/04656
CC FILING DATE:
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Gordon, Alan M.
CC REGISTRATION NUMBER: 30, 637
CC REFERENCE/DOCKET NUMBER: 32, 390-00/PCT
CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: 201-831-3244
CC TELEFAX: 201-831-3305
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 990 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 990 AA; 111713 MW; 5013050 CN;

DB 10; Score 79; Match 32.1%; QryMatch 4.8%; Pred. No. 1.32e+01;
Matches 17; Conservative 12; Mismatches 22; Indels 2; Gaps 2;

Db 273 GV-FSEGTQKALIDANMLRDVGKTLTQTATYLRSDLSATDRKKLEERYLLG 323
QY 99 GVSIDVGKKEYLIAGKAGDGRMHITLDFIVPDTLSTQKSLNHRQMG 151

RESULT 6
ID PCT-US94-06430-12 STANDARD; PRT; 476 AA.
XX AC xxxxxx
XX 01-JAN-1900
DE Sequence 12, Application PC/TUS9406430.
XX Sequence 12, Application PC/TUS9406430
CC GENERAL INFORMATION:
CC APPLICANT: The Upjohn Company
CC TITLE OF INVENTION: Lettuce Infectious Yellow Virus Genes
CC NUMBER OF SEQUENCES: 25
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Upjohn Company, Corp. Intellectual
CC ADDRESSEE: Property Law
CC STREET: 301 Henrietta Street
CC CITY: Kalamazoo
CC STATE: Michigan
CC COUNTRY: USA
CC ZIP: 49001
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/06430
CC FILING DATE:
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Darnley Jr., James D.
CC REGISTRATION NUMBER: 33,673
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 616-385-5210
CC TELEFAX: 616-385-6897
CC TELEX: 224401
CC INFORMATION FOR SEQ ID NO: 12:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 476 amino acids
CC TYPE: amino acid

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CC STRANDEDNESS: single
CC TOPOLOGY: linear
CSQ SEQUENCE 476 AA; 53506 MW; 1217402 CN;
DB 9; Score 79; Match 39.5%; QryMatch 4.8%; Pred. No. 1.32e+01;
Matches 17; Conservative 7; Mismatches 14; Indels 5; Gaps 3;
Ddb 256 YEEMMYKMGFGSPELYDRDFKYTFYFCRAKATCGVDLELGTQR 298
   ||| ||| :|| |:||| : ||| ||| :||| :
Qy 71 YEIKQIKMFK-GPEK-DIEFIYTA---PSSAVCGVSLDVGKK 108
RESULT 7
ID PCT-US95-06119-14 STANDARD; PRT; 397 AA.
XX
XX xxxxxx
XX 01-JAN-1900
XX
XX Sequence 14, Application PC/TUS9506119.
XX
XX Sequence 14, Application PC/TUS9506119
XX GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE CAPSULAR
CC TITLE OF INVENTION: POLYSACCHARIDE GENES AND FLANKING REGIONS
CC NUMBER OF SEQUENCES: 20
CC CORRESPONDENCE ADDRESS:
CC ADDRESS: Arnold, White & Durkee
CC CITY: Houston
CC STATE: TX
CC COUNTRY: United States of America
CC ZIP: 77210
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
CC SOFTWARE: PatentIn Release #1.0, Version
CC SOFTWARE: #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/06119
CC FILING DATE: CONCURRENTLY HERewith
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/243,546
CC FILING DATE: 16-MAY-1994
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Parker, David L.
CC REGISTRATION NUMBER: 32,165
CC REFERENCE/DOCKET NUMBER: AMCY018P--
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (512) 418-3000
CC TELEFAX: (713) 789-2679
CC TELEX: 79-0924
CC INFORMATION FOR SEQ ID NO: 14:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 397 amino acids
CC TYPE: amino acid
CC

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CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 397 AA; 43352 MW; 781935 CN;
DB 10; Score 79; Match 26.1%; QryMatch 4.8%; Pred. No. 1.32e+01;
Matches 12; Conservative 13; Mismatches 19; Indels 2; Gaps 2;
Db 347 AKSIVSTELVTKIAESYGPECLTSLQVSNLSLRKFKNLKKNTVMF 392
|:: | | : ||: | : ||: ||: |::| |::|
QY 47 AKAVSEKE-VDSGNDIYNP-IKRIQYEIKQIKMFKGEKDIEFIY 90

RESULT      8
ID PCT-US94-10357-3 STANDARD; PRT; 928 AA.
XX xxxxxx
XX
XX 01-JAN-1900
XX
XX Sequence 3, Application PC/TUS9410357.
DE
XX
CC Sequence 3, Application PC/TUS9410357
CC GENERAL INFORMATION:
CC APPLICANT: The Regents of the University of California
CC APPLICANT: and Ganji, Inc.
CC TITLE OF INVENTION: Therapeutic Use of the Retinoblastoma
CC TITLE OF INVENTION: Susceptibility Gene Product
CC NUMBER OF SEQUENCES: 3
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Campbell and Flores
CC STREET: 4370 La Jolla Village Drive
CC CITY: San Diego
CC STATE: California
CC COUNTRY: USA
CC ZIP: 92122
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/10357
CC FILING DATE: 13-SEP-1994
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/121,108
CC FILING DATE: 13-SEP-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Campbell, Cathryn A.
CC REGISTRATION NUMBER: 31,815
CC REFERENCE/DOCKET NUMBER: FP-UC 1117
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (619) 535-9001
CC TELEFAX: (619) 535-8949
CC INFORMATION FOR SEQ ID NO: 3:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 928 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
```


CC LENGTH: 490 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC HYPOTHETICAL: YES
SQ SEQUENCE 490 AA; 55708 MW; 1357717 CN;
DB 10; Score 74; Match 25.6%; QryMatch 4.5%; Pred. No. 3.00e+01;
Matches 21; Conservative 20; Mismatches 37; Indels 4; Gaps 4;
Db 1 MDPXV-VLVLCISLLSLWROSGRGKLPGLPPTLPXIGNILQIDKDIS-KSLFNXS 58
Qy 1 MGAARTLRALGLLLLATILRPADACSPVHPQQAFCNADVV-IRAKAVSEKVDSGN 59
Db 59 KVIYG-PVFTFYFGLKPIVVLHG 79
Qy 60 DIYGNPIKRIQYKIKMFKG 81

RESULT 11
ID PCT-US93-03076-4 STANDARD; PRT; 778 AA.

XX AC xxxxxx

XX DT 01-JAN-1900

XX Sequence 4, Application PC/TUS9303076.

CC Sequence 4, Application PC/TUS9303076

CC GENERAL INFORMATION:

CC APPLICANT: Whitehead Institute for Biomedical Research

CC TITLE OF INVENTION: GAP-Associated Protein p190 and

CC TITLE OF INVENTION: Transduction

CC NUMBER OF SEQUENCES: 20

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

CC STREET: 2 Militia Drive

CC CITY: Lexington

CC STATE: MA

CC COUNTRY: US

CC ZIP: 02173

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patent in Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: PCT/US93/03076

CC FILING DATE: 19930331

CC CLASSIFICATION:

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Granahan, Patricia

CC REGISTRATION NUMBER: 32,227

CC REFERENCE/DOCKET NUMBER: WHI92-03A

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: 617-861-6240

CC TELEFAX: 617-861-9540

CC INFORMATION FOR SEQ ID NO: 4:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 778 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 778 AA; 87981 MW; 3142889 CN;
DB 8; Score 74; Match 24.3%; QryMatch 4.5%; Pred. No. 3.00e+01;
Matches 17; Conservative 12; Mismatches 37; Indels 4; Gaps 4;
Db 159 KHIHFVH-PKTCPCPCACVDAKIEHLISSRFIRPSDRNQKNSLSDPNIDRLNVLIG 217
Qy 84 KDIEFIYTPASSAVCGVSLD-VGGKKEYLIAGK-AEGDGKMH-I-TLCDFIVPMDTILSTTQ 140
Db 218 KDALPESWPM 227
Qy 141 KKSILNHYQM 150

RESULT 12
ID US-07-803-636A-2 STANDARD; PRT; 480 AA.

XX AC xxxxxx

XX DT 01-JAN-1900

XX Sequence 2, Application US/07803636A.

XX Sequence 2, Application US/07803636A

CC GENERAL INFORMATION:

CC APPLICANT: MCGUIRE, TRAVIS C., TERRY F. McELWAIN, LANCE E. PERRYMAN,

CC APPLICANT: WILLIAM C. DAVIS

CC TITLE OF INVENTION: IMMUNIZATION AGAINST BABESIOSIS USING

CC TITLE OF INVENTION: PURIFIED SURFACE ANTIGENS OF BABESIA BIGEMINA AND

CC SIMILAR

CC TITLE OF INVENTION: IMMUNOGENS

CC NUMBER OF SEQUENCES: 2

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: DAVID R. SALIWANCHIK

CC STREET: 2421 NW 41ST STREET, SUITE A-1

CC CITY: GAINESVILLE

CC STATE: FLORIDA

CC COUNTRY: USA

CC ZIP: 32606

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patent in Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/07/803,636A

CC FILING DATE: 19911206

CC CLASSIFICATION: 424

CC ATTORNEY/AGENT INFORMATION:

CC NAME: SALIWANCHIK, DAVID R

CC REGISTRATION NUMBER: 31,794

CC REFERENCE/DOCKET NUMBER: WA4-059.C1

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: 904-375-8100

CC TELEFAX: 904-372-5800

CC INFORMATION FOR SEQ ID NO: 2:

QY 47 AKAVSEKVDGNDIYGNPKRIQYEIKQIKMKFGPKDI 86
::||: :: |||| |:: || | ::|| ::||
RESULT 14
ID PCT-US95-05008-8 STANDARD; PRT; 659 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 8, Application PC/TUS9505008.
XX
CC Sequence 8, Application PC/TUS9505008
CC GENERAL INFORMATION:
CC APPLICANT: Sugen, Inc.
CC APPLICANT: 515 Galveston Drive
CC APPLICANT: Redwood City, California 94063-4720
CC APPLICANT: United States of America
CC APPLICANT: Wissenschaften E.V.
CC APPLICANT: Hofgarten Str. 2
CC APPLICANT: Munchen 80539
CC APPLICANT: Germany
CC TITLE OF INVENTION: Novel Megakaryocytic Protein Tyrosine
CC TITLE OF INVENTION: Kinases
CC NUMBER OF SEQUENCES: 21
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Pennie & Edmonds
CC STREET: 1155 Avenue of the Americas
CC CITY: New York
CC STATE: New York
CC COUNTRY: U.S.A.
CC ZIP: 10036
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/05008
CC FILING DATE: 24-APR-1995
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/232,545
CC FILING DATE: 22-APR-1994
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Coruzzi, Laura A.
CC REGISTRATION NUMBER: 30,742
CC REFERENCE/DOCKET NUMBER: 7683-074
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212) 790-9090
CC TELEFAX: (212) 869-9741
CC TELEX: 66141 PENNIE
CC INFORMATION FOR SEQ ID NO: 8:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 659 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: unknown
CC TOPOLOGY: unknown

CC MOLECULE TYPE: protein
SQ SEQUENCE 659 AA; 76281 MW; 2353510 CN;
DB 10; Score 71; Match 47.8%; QryMatch 4.3%; Pred. No. 4.86e+01;
Matches 11; Conservative 5; Mismatches 5; Indels 2; Gaps 2;
Db 422 RGQYDV-AIKMIKEGSMSEDEFI 443
| ||: |||| |:: || | ::|| ::||
QY 68 RIQYEIKQIKMKF-GPEKDIEFI 89
XX
DE Sequence 1, Application PC/TUS9301652.
XX
CC Sequence 1, Application PC/TUS9301652
CC GENERAL INFORMATION:
CC APPLICANT: Bouck, Noel P.
CC APPLICANT: Polverini, Peter J.
CC APPLICANT: Good, Deborah J.
CC APPLICANT: Frazier, William A.
CC TITLE OF INVENTION: Method and Composition for
CC TITLE OF INVENTION: Inhibiting Angiogenesis
CC NUMBER OF SEQUENCES: 12
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut
CC STREET: 100 South Wacker Drive, Suite 960
CC CITY: Chicago
CC STATE: Illinois
CC COUNTRY: USA
CC ZIP: 60606-4002
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US93/01652
CC FILING DATE: 19930222
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US/07/841,656
CC FILING DATE: 24-FEB-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US/07/464,369
CC FILING DATE: 12-JAN-1990
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fentress, Susan B.
CC REGISTRATION NUMBER: 31,327
CC REFERENCE/DOCKET NUMBER: 92005-PCT
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (312)-456-8000
CC TELEFAX: (312)-456-7776
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 239 amino acids
CC TYPE: AMINO ACID
CC STRANDEDNESS: unknown
CC TOPOLOGY: unknown
CC MOLECULE TYPE: peptide
SQ SEQUENCE 239 AA; 26213 MW; 275594 CN;

DB 8; Score 70; Match 47.6%; QryMatch 4.3%; Pred. No. 5.70e+01;
Matches 10; Conservative 4; Mismatches 5; Indels 2; Gaps 2;

Ds 37 CKKVCPIPCSNATVPDGE 57
QY 154 CKITRCPIPCYISS-PD-EC 172

Search completed: Mon Feb 5 17:01:42 1996
Job time : 10 secs.

W P S R E L H (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MParch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Mon Feb 5 17:02:03 1996; MacPar time 13.15 Seconds
Tabular output not generated. 195.746 Million cell updates/sec

Title: >FIG2
Description: (1:220) from trans.pep
Perfect Score: 1643
Sequence: 1 MGAARTLRALGLLLATL.....CAWYRGAAPPKQEFIDIEDP 220

Scoring table: PAM 150
Gap 11

Searched: 131564 seqs, 11696421 residues

Database: a-pending

- 1 PCT91
- 2 PCT92
- 3 PCT93
- 4 PCT94
- 5 PCT95
- 6 PCT96
- 7 U73
- 8 U74
- 9 U75
- 10 U76

11 U771
12 U772
13 U781
14 U782
15 U791
16 U792
17 U800
18 U801
19 U802
20 U803
21 U804
22 U805
23 U806
24 U807
25 U808
26 U809
27 U810
28 U811
29 U812
30 U813
31 U814
32 U815
33 U816
34 U817
35 U818
36 U819
37 U820
38 U821
39 U822
40 U823
41 U824
42 U825
43 U826
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45 U828
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51 U834
52 U835
53 U836
54 U837
55 U838
56 U839
57 U840
58 U841
59 U842
60 U843
61 U844
62 U845
63 U846
64 U847
65 U848
66 U849
67 U85
68 U60
69 NEWP
70 NEW08

Statistics: Mean 30.214; Variance 114.839; scale 0.263

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1643	100.0	220	33	US-08-167-Sequence 10, Applicati	1.12e-168
2	1607	97.8	220	33	US-08-167-Sequence 11, Applicati	1.24e-164
3	1550	94.3	220	33	US-08-167-Sequence 12, Applicati	3.16e-158
4	844	51.4	224	4	PCT-US94-1Sequence 2, Applicatio	2.19e-79
5	695	42.3	211	4	PCT-US94-1Sequence 13, Applicati	6.06e-63
6	695	42.3	211	4	PCT-US94-1Sequence 13, Applicati	6.06e-63
7	695	42.3	211	4	PCT-US94-1Sequence 2, Applicatio	6.06e-63
8	695	42.3	211	4	PCT-US94-1Sequence 2, Applicatio	6.06e-63
9	686	41.8	212	33	US-08-167-Sequence 13, Applicati	5.91e-62
10	686	41.8	211	33	US-08-167-Sequence 14, Applicati	5.91e-62
11	685	41.7	198	33	US-08-134-Sequence 15, Applicati	7.61e-62
12	685	41.7	198	33	US-08-134-Sequence 15, Applicati	7.61e-62
13	673	41.0	188	33	US-08-167-Sequence 1, Applicatio	1.58e-60
14	556	33.8	164	30	US-08-134-Sequence 17, Applicati	9.90e-48
15	556	33.8	164	4	PCT-US94-1Sequence 17, Applicati	9.90e-48
16	521	31.7	207	33	US-08-167-Sequence 6, Applicatio	6.31e-44
17	518	31.5	206	33	US-08-167-Sequence 7, Applicatio	1.33e-43
18	517	31.5	205	33	US-08-167-Sequence 4, Applicatio	1.71e-43
19	506	30.8	205	33	US-08-167-Sequence 8, Applicatio	2.67e-42
20	488	29.7	207	33	US-08-167-Sequence 9, Applicatio	2.37e-40
21	476	29.0	207	33	US-08-167-Sequence 5, Applicatio	4.69e-39
22	470	28.6	125	33	US-08-167-Sequence 16, Applicati	2.08e-38
23	219	13.3	28	65	US-08-488-Sequence 245, Applicat	5.29e-12
24	219	13.3	28	65	US-08-488-Sequence 245, Applicat	5.29e-12
25	219	13.3	28	24	US-08-077-Sequence 245, Applicat	5.29e-12
26	219	13.3	28	24	US-08-077-Sequence 245, Applicat	5.29e-12
27	219	13.3	28	65	US-08-488-Sequence 245, Applicat	5.29e-12
28	219	13.3	28	64	US-08-476-Sequence 245, Applicat	5.29e-12
29	219	13.3	28	64	US-08-476-Sequence 245, Applicat	5.29e-12
30	219	13.3	28	64	US-08-475-Sequence 245, Applicat	5.29e-12
31	157	9.6	19	63	US-08-488-Sequence 246, Applicat	6.71e-06
32	157	9.6	19	63	US-08-488-Sequence 246, Applicat	6.71e-06
33	157	9.6	19	64	US-08-475-Sequence 246, Applicat	6.71e-06
34	157	9.6	19	64	US-08-475-Sequence 246, Applicat	6.71e-06
35	157	9.6	19	65	US-08-480-Sequence 246, Applicat	6.71e-06
36	157	9.6	19	65	US-08-487-Sequence 246, Applicat	6.71e-06
37	157	9.6	19	24	US-08-077-Sequence 246, Applicat	6.71e-06
38	157	9.6	19	24	US-08-077-Sequence 246, Applicat	6.71e-06
39	138	8.4	25	64	US-08-474-Sequence 21, Applicatio	4.16e-04
40	131	8.0	18	33	US-08-167-Sequence 21, Applicati	1.85e-03
41	117	7.1	18	33	US-08-167-Sequence 18, Applicati	3.45e-02
42	116	7.1	18	33	US-08-167-Sequence 19, Applicati	4.24e-02
43	100	6.1	28	31	US-08-141-Sequence 1, Applicatio	1.06e+00
44	99	6.0	18	33	US-08-167-Sequence 20, Applicati	1.29e+00
45	96	5.8	76	67	US-08-538-Sequence 4, Applicatio	2.32e+00

ALIGNMENTS

RESULT 1
ID US-08-167-463-10 STANDARD; PRT; 220 AA.

XX xxxxxx

XX 01-JAN-1900

XX Sequence 10, Application US/08167463.

CC Sequence 10, Application US/08167463
GENERAL INFORMATION:

CC APPLICANT: HAWKES, SUSAN P.

CC APPLICANT: KISHANI, NARENDRA S.

CC APPLICANT: YANG, TE-TUAN

CC TITLE OF INVENTION: HUMAN TIMP-3

CC NUMBER OF SEQUENCES: 32

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: MORRISON & FOERSTER

CC STREET: 755 Page Mill Road

CC CITY: Palo Alto

CC STATE: California

CC COUNTRY: USA

CC ZIP: 94304-1018

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patent In Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/167,463

CC FILING DATE: 13-DEC-1993

CC CLASSIFICATION: 530

CC ATTORNEY/AGENT INFORMATION:

CC NAME: LEHNHARDT, SUSAN K.

CC REGISTRATION NUMBER: 33,943

CC REFERENCE/DOCKET NUMBER: 22000-20542.20

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (415) 813-5600

CC TELEFAX: (415) 494-0792

CC TELEX: 706141

CC INFORMATION FOR SEQ ID NO: 10:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 220 amino acids

CC TYPE: amino acid

CC STRANDEDNESS: single

CC TOPOLOGY: linear

CC SEQUENCE 220 AA; 24399 MW; 242975 CN;

DB 33; Score 1643; Match 100.0%; QryMatch 100.0%; Pred. No. 1.12e-168; Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MCAARTLRALGILLATLRPADACSPVHPQQAFQADVVIRAKVSEKVDSDND 60

QY 1 MCAARTLRALGILLATLRPADACSPVHPQQAFQADVVIRAKVSEKVDSDND 60

Db 61 IYGNPKRIQVEIKQKMGKPEKIDIEFIYTPASSAVCGVSLDVGGKKEYLIAGKAGSDG 120

QY 61 IYGNPKRIQVEIKQKMGKPEKIDIEFIYTPASSAVCGVSLDVGGKKEYLIAGKAGSDG 120

BONET PROXY

Db 121 KMHTLCLDFIVPMDTSTTQKSLNHRVOMGCECKITRCMPICVYISSPDECLMDWVTE 180
Qy 121 KMHTLCLDFIVPMDTSTTQKSLNHRVOMGCECKITRCMPICVYISSPDECLMDWVTE 180
Db 181 KNINGHOAKFFACIKRSDGSCAWYRGAPPKQEFFLDIEDP 220
Qy 181 KNINGHOAKFFACIKRSDGSCAWYRGAPPKQEFFLDIEDP 220

RESULT 2
ID US-08-167-463-11 STANDARD; PRT; 220 AA.

XX xxxxxx

XX 01-JAN-1900

XX Sequence 11, Application US/08167463.

XX Sequence 11, Application US/08167463

CC GENERAL INFORMATION:

CC APPLICANT: HAWKES, SUSAN P.

CC APPLICANT: KISHNANI, NARENDRA S.

CC APPLICANT: YANG, TE-TUAN

CC TITLE OF INVENTION: HUMAN TIMP-3

CC NUMBER OF SEQUENCES: 32

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: MORRISON & FOERSTER

CC STREET: 755 Page Mill Road

CC CITY: Palo Alto

CC STATE: California

CC COUNTRY: USA

CC ZIP: 94304-1018

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patent In Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/167,463

CC FILING DATE: 13-DEC-1993

CC CLASSIFICATION: 530

CC ATTORNEY/AGENT INFORMATION:

CC NAME: LEHNHARDT, SUSAN K.

CC REGISTRATION NUMBER: 33,943

CC REFERENCE/DOCKET NUMBER: 22000-20542.20

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (415) 813-5600

CC TELEFAX: (415) 494-0792

CC TELEX: 706141

CC INFORMATION FOR SEQ ID NO: 11:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 220 amino acids

CC TYPE: amino acid

CC STRANDEDNESS: single

CC TOPOLOGY: linear

CC SEQUENCE 220 AA; 24367 MW; 243101 CN;

DB 33; Score 1607; Match 96.8%; QryMatch 97.8%; Pred. No. 1.24e-164;
Matches 213; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 1 MGAARSURLAHGLLLASLLRPADACSPVHPQOAFCNADVIRAKAVSEKEVDSGND 60
Qy 1 MGAARSURLAHGLLLASLLRPADACSPVHPQOAFCNADVIRAKAVSEKEVDSGND 60
Db 61 IYGNPKRIQYIEIKRMFKGPKDIEFIYAPSSAVCGVSLDVGKKEYLIAGKAEGDG 120
Qy 61 IYGNPKRIQYIEIKRMFKGPKDIEFIYAPSSAVCGVSLDVGKKEYLIAGKAEGDG 120
Db 121 KMHTLCLDFIVPMDTSTTQKSLNHRVOMGCECKITRCMPICVYISSPDECLMDWVTE 180
Qy 121 KMHTLCLDFIVPMDTSTTQKSLNHRVOMGCECKITRCMPICVYISSPDECLMDWVTE 180
Db 181 KNINGHOAKFFACIKRSDGSCAWYRGAPPKQEFFLDIEDP 220
Qy 181 KNINGHOAKFFACIKRSDGSCAWYRGAPPKQEFFLDIEDP 220

RESULT 3
ID US-08-167-463-12 STANDARD; PRT; 220 AA.

XX xxxxxx

XX 01-JAN-1900

XX Sequence 12, Application US/08167463.

XX Sequence 12, Application US/08167463

CC GENERAL INFORMATION:

CC APPLICANT: HAWKES, SUSAN P.

CC APPLICANT: KISHNANI, NARENDRA S.

CC APPLICANT: YANG, TE-TUAN

CC TITLE OF INVENTION: HUMAN TIMP-3

CC NUMBER OF SEQUENCES: 32

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: MORRISON & FOERSTER

CC STREET: 755 Page Mill Road

CC CITY: Palo Alto

CC STATE: California

CC COUNTRY: USA

CC ZIP: 94304-1018

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patent In Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/167,463

CC FILING DATE: 13-DEC-1993

CC CLASSIFICATION: 530

CC ATTORNEY/AGENT INFORMATION:

CC NAME: LEHNHARDT, SUSAN K.

CC REGISTRATION NUMBER: 33,943

CC REFERENCE/DOCKET NUMBER: 22000-20542.20

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (415) 813-5600

CC TELEFAX: (415) 494-0792

CC TELEX: 706141

CC INFORMATION FOR SEQ ID NO: 12:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 220 amino acids

CC	TYPE: amino acid	
CC	STRANDEDNESS: single	
CC	TOPOLOGY: linear	
CC	SEQUENCE	220 AA; 24355 MW; 234318 CN;
DB 33;	Score	1550; Match 91.8%; QryMatch 94.3%; Pred. No. 3.16e-158;
Matches	Conservative	12; Mismatches 6; Indels 0; Gaps 0;
Db	1	MGAARSPLAFPCILLGLTLLPRADSCSPVHPQOAFCDNADIVIRAKAVNKKEVDSGND 60
Qy	1	MGAAARTLRLALGLLLATLRLPADACSCSPVHPQOAFCDNADVIRAKAVSEKVEDSGND 60
Db	61	IYGNPIKRIQIEIKQIKMFKCPDODIEFIYTAPAAVCGVSLDIGGKEYILLIAGKAEKNG 120
Qy	61	IYGNPIKRIQIEIKQIKMFKGPKEJEFITYAPSSAVCGVSLDVGGKEYILLIAGKAEKGD 120
Db	121	NMHITLCLDFIVPWTLSATOKKSLNHRYQMGCECKITRCMPICVYISSPDECLMDWVTE 180
Qy	121	NMHITLCLDFIVPWTLSSTQKSLNHRYQMGCECKITRCMPICVYISSPDECLMDWVTE 180
Db	181	KNINGHOAKFFACIKRSGSCAWYGAAPPKQEFIDIEDP 220
Qy	181	KNINGHOAKFFACIKRSGSCAWYGAAPPKQEFIDIEDP 220
RESULT	4	
ID	PCT-US94-14498A-2	STANDARD; PRT; 224 AA.
XX	xxxxxx	
XX	01-JAN-1900	
XX		
XX		
XX		
CC	Sequence 2, Application PC/TUS9414498A.	
CC	GENERAL INFORMATION:	
CC	APPLICANT: GREENE, ET AL.	
CC	TITLE OF INVENTION: Human TIMP-4	
CC	NUMBER OF SEQUENCES: 2	
CC	CORRESPONDENCE ADDRESS:	
CC	ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLIAN,	
CC	ADDRESSEE: CECCHI, STEWART & OLSTEIN	
CC	STREET: 6 BECKER FARM ROAD	
CC	CITY: ROSELAND	
CC	STATE: NEW JERSEY	
CC	COUNTRY: USA	
CC	ZIP: 07068	
CC	COMPUTER READABLE FORM:	
CC	MEDIUM TYPE: 3.5 INCH DISKETTE	
CC	COMPUTER: IBM PS/2	
CC	OPERATING SYSTEM: MS-DOS	
CC	SOFTWARE: WORD PERFECT 5.1	
CC	CURRENT APPLICATION DATA:	
CC	APPLICATION NUMBER: PCT/US94/14498A	
CC	FILING DATE: Submitted herewith	
CC	CLASSIFICATION:	
CC	PRIOR APPLICATION DATA:	
CC	APPLICATION NUMBER:	
CC	FILING DATE:	
CC	ATTORNEY/AGENT INFORMATION:	

```

CC NAME: FERRARO, GREGORY D.
CC REGISTRATION NUMBER: 36,134
CC REFERENCE/DOCKET NUMBER: 325800-278
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 201-994-1700
CC TELEFAX: 201-994-1744
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 224 AMINO ACIDS
CC TYPE: AMINO ACID
CC STRANDEDNESS:
CC TOPOLOGY: LINEAR
CC MOLECULE TYPE: PROTEIN
CC SEQUENCE 224 AA; 25502 MW; 274373 CN;

DB 4; Score 844; Match 48.2%; OryMatch 51.4%; Pred. No. 2,19e-79;
Matches 109; Conservative 53; Mismatches 56; Indels 8; Gaps 5;

Db 1 MPGSPRPAP--SWLLLLLLRLLPPGLGEACSCAPAHPOQHCHTSALVIRAKISSEKVP 59
|:::| |::| |::| |::| |::| |::| |::| |::| |::| |
Qy 1 MGAARTIRLALGLLL-LATLRPA---DACSCSPVHPQQAFCNADVVIRAKVSEKVD 56

Db 60 ASADP-ADTERMLRYEIKQIKMFGFKYKDVQYIYTPDFDSLGVKLEANSQKQYLLTG 118
|:::| |::| |::| |::| |::| |::| |::| |::| |::| |
Qy 57 SGNDIYGNPIRKRIQYIEIKIMFKGPEK--DIEFIYTPSSAVCGSLDVGKREYLIAG 114

Db 119 QVLSDGKGFILHLCNVIEPWEDSLIVQRESLNHHYHLNCGQITTCYTPVCTISAPNECLW 178
|:::| |::| |::| |::| |::| |::| |::| |::| |::| |
Qy 115 KAEGDGKMHITLUCDFIVPMDTFLSTQKKSLNHRIQMGCECKITRCMPICYSFDECLW 174

Db 179 TDWLLERLYGQAOHYVCKMKHVDGTCGWSYRGHLPLRKFEVDIVQ 224
|::| |::| |::| |::| |::| |::| |::| |::| |::| |
Qy 175 MDWVTEKNGHQAKFFACIKRSDGSCAWYRGAAPKQFFLIEDP 220

RESULT 5
ID PCT-US94-11241-13 STANDARD; PRT; 211 AA.

```

RESULT	5			
ID	PC-TUS94-11241-13	STANDARD;	PRT;	211 AA.
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XX	XX			
DT	01-JAN-1900			
XX				
DE	Sequence 13, Application PC/TUS9411241.			
XX				
CC	Sequence 13, Application PC/TUS9411241			
CC	GENERAL INFORMATION:			
CC	APPLICANT: Silbiger, Scott M.			
CC	APPLICANT: Koski, Raymond A.			
CC	TITLE OF INVENTION: Tissue Inhibitor Metalloproteinase Type			
CC	TITLE OF INVENTION: Three (TIMP-3) Composition and Methods			
CC	NUMBER OF SEQUENCES: 21			
CC	CORRESPONDENCE ADDRESS:			
CC	ADDRESS: Amgen Inc./Patent Operations/KMP			
CC	STREET: 1840 Dehavilland Drive			
CC	CITY: Thousand Oaks			
CC	STATE: California			
CC	COUNTRY: USA			
CC	ZIP: 91320-1789			
CC	COMPUTER READABLE FORM:			
CC	MEDIUM TYPE: Floppy disk			
CC				

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/11241
FILING DATE:
CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 211 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 211 AA; 24145 MW; 244095 CN;

DB	4;	Score	695;	Match	43.6%;	QtyMatch	42.3%;	Pred.	No.	6.06e-63;	
		Matches	99;	Conservative	56;	Mismatches	55;	Indels	12;	Gaps	10;
Db			2	TPWLGLIVLLGSWSLDGWAEGACETSPSHQDPAFNSDIVIRAKVVGKKLVKEGP--FGT	59						
Qy			7	TIRLALGILLIA-TLL-RPADAGSCSEVFPQAFQADVWIRAKAVSEKEVDSGNDIYGN	64						
Db			60	-L--V-YTIKQMKRYGFTKMPHVIQYIHTAEASGLCKLEVN-KYQYLLITGRVY-DGKM	113						
Qy			65	PIKRIQEIKQIKMFKG-PEK-DIEFIYIAPSSAVCGVSLDVGGKKEYIAGAEQDGKM	122						
Db			114	YTGICNFVERMDQITLSQKGLNRYRHLGCNKKIKSCYYILPCFTVSKNECLWTDMLSNFG	173						
Qy			123	HTIGDFTVPMDITLSTTKKSLNHRVOMGECKITRCPMIFCIYSSPECLMMDWVTEKN	182						
Db			174	YPGYSKHYACIRQKGYCSWYRGWAPPDKSIINATDP	211						
Qy			183	INGHOAKFFACIKRSDGSCAWYRGGAAPPKQEFLDIEDP	220						

[illegible]

CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0.
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/134,231
CC FILING DATE:
CC CLASSIFICATION: 424
CC INFORMATION FOR SEQ ID NO: 13:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 211 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 211 AA: 24145 MW: 244095 CN:

DB 30; Matches	Score 95;	Match 43.6%;	QryMatch 42.3%;	Pred. No. 6.06e-63;	Indels 12;	Gaps 10;
Db	95;	Match 43.6%;	QryMatch 42.3%;	Pred. No. 6.06e-63;	Indels 12;	Gaps 10;
Db	2	TPWLGLIVLLGSWSLGDWGAECTCSPHPQDAFCNSDIVIRAKVVGKKLYKEGP--FGT	59			
Qy	7	TLRLALGLLLLA-TLL-RPADACSCSPVHPQQAFCNADVVIRAKAVSEKEVDSGNDIYGN	64			
Db	60	-L--V-YTIKQMKYRGFTKMPHVYTHTEASESLGCLKEVN-KYQYTLGTVYV-DGKM	113			
Qy	65	PIKRIQYEIKQIKMEFG-PEK-DIEFIYITAPSAVCGSLDVGGKKEYLIAGKAEGDGKM	122			
Db	114	YTGICNFVERWDQILTSORGLNRYVHLGNCNCKIKSCYYLPFCVTSKNECLWTLMDLSNFG	173			
Qy	123	HTFLDGFVPMDDTLSTQKSLNHRHYOMGCEKTLRCPMIPCIYSSPDECLMMDWVTEKN	182			
Db	174	YFGYSKHYACIROGGYGCYSWRGAWPPDKSIINATDP	211			
Qy	183	INGHOAKFFACIKSDSGSCAWYRGAPPKQEFFLDIEDP	220			

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ID	PCT-US94-11599-2	STANDARD;	PRT;	211	AA.
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AC	XXXXXX				
XX					
DT	01-JAN-1900				
XX					
DE	Sequence 2, Application PC/TUS9411599.				
XX					
CC	Sequence 2, Application PC/TUS9411599				
CC	GENERAL INFORMATION:				
CC	APPLICANT: Incyte Pharmaceuticals, Inc.				
CC	APPLICANT: 3330 Hillview Avenue				
CC	APPLICANT: Palo Alto, California 94304				
CC	APPLICANT: United States of America				
CC	TITLE OF INVENTION: Novel Human Monocyte/Mac				
CC	TITLE OF INVENTION: Metalloproteinase Inhibi				
ses					
CC	NUMBER OF SEQUENCES: 6				
CC	CORRESPONDENCE ADDRESS:				
CC	ADDRESSEE: Pennie and Edmonds				
CC	STREET: 1155 Avenue of the Americas				
CC	CITY: New York				

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CC STATE: California
CC COUNTRY: United States of America
CC ZIP: 10036
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/11599
CC FILING DATE: 07-OCT-1994
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Halluin, Albert P.
CC REGISTRATION NUMBER: 25,227
CC REFERENCE/DOCKET NUMBER: 8135-041
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-854-3660
CC TELEFAX: 415-854-3694
CC TELEX: 66141 PENNIE
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 211 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: unknown
CC TOPOLOGY: unknown
CC MOLECULE TYPE: protein
CC IMMEDIATE SOURCE:
CC CLONE: T-012006
CC SEQUENCE 211 AA; 24145 MW; 244095 CN;

DB 4; Score 695; Match 43.6%; QryMatch 42.3%; Pred. No. 6.06e-63;
Matches 95; Conservative 56; Mismatches 55; Indels 12; Gaps 10;

Db 2 TPWLGLVLVLSGSLGWGAECTSPSHQDAFCNSDIVIRAKVVGKLVKEGP--FGT 59
Qy 7 TLRALGLLLLA-TLL-RPADACSCSPVHPQQAFCNADVVIRAKAVSEKVEDSGNDIYN 64

Db 60 -L--V-YTIKQMKYRGFTKMPHVQYIHTASESLCGKLEVN-KYQYLITGRVY-DGKM 113
Qy 65 PIKRIQVEIKQIKMFKG-PEK-DIEFIYTPSSAVCGVSLDVGGKKEVLIAGKAEKGDM 122
Db 114 YTGCLNFERWDQLTLSQRKGLNRYHLGCNCKIKSCYILPCFVTSKNECLWTDMLSNFG 173
Qy 123 HITLCDFIVPWDTLTSTQKSLNHRVQMGCECKITRCMPICYSISPDECLWMDWVTEKN 182

Db 174 YPGYQSKHACIRQKGGYCSWYRGWAPDPKSIINATDP 211
Qy 183 INGHQAKFACIKRSDGSCAWYRGAAAPKPFLEIDEDP 220

RESULT 8
ID US-08-319-555-2 STANDARD; PRT; 211 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
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DE Sequence 2, Application US/08319555.
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CC Sequence 2, Application US/08319555
CC GENERAL INFORMATION:
CC APPLICANT: Scott, Randal W.
CC APPLICANT: Levine, Wendy B.
CC APPLICANT: Seilhamer, Jeffrey J.
CC APPLICANT: Delegeane, Angelo M.
CC TITLE OF INVENTION: Novel Human Monocyte/Macrophage Derived
CC TITLE OF INVENTION: Metalloproteinase Inhibitor, Its Production And U
ses
CC NUMBER OF SEQUENCES: 4
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Pennie & Edmonds
CC STREET: 1155 Avenue of the Americas
CC CITY: New York
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 10036
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/319,555
CC FILING DATE: 07-OCT-1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/133,956
CC FILING DATE: 07-OCT-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Halluin, Albert P.
CC REGISTRATION NUMBER: 25,227
CC REFERENCE/DOCKET NUMBER: 8135-041-999
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-854-3660
CC TELEFAX: 415-854-3694
CC TELEX: 66141 PENNIE
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 211 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 211 AA; 24145 MW; 244095 CN;

DB 48; Score 695; Match 43.6%; QryMatch 42.3%; Pred. No. 6.06e-63;
Matches 95; Conservative 56; Mismatches 55; Indels 12; Gaps 10;

Db 2 TPWLGLVLVLSGSLGWGAECTSPSHQDAFCNSDIVIRAKVVGKLVKEGP--FGT 59
Qy 7 TLRALGLLLLA-TLL-RPADACSCSPVHPQQAFCNADVVIRAKAVSEKVEDSGNDIYN 64

Db 60 -L--V-YTIKQMKYRGFTKMPHVQYIHTASESLCGKLEVN-KYQYLITGRVY-DGKM 113
Qy 65 PIKRIQVEIKQIKMFKG-PEK-DIEFIYTPSSAVCGVSLDVGGKKEVLIAGKAEKGDM 122
Db 114 YTGCLNFERWDQLTLSQRKGLNRYHLGCNCKIKSCYILPCFVTSKNECLWTDMLSNFG 173
Qy 123 HITLCDFIVPWDTLTSTQKSLNHRVQMGCECKITRCMPICYSISPDECLWMDWVTEKN 182
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DB 33; Score Matches	686; Match 43.1%; 94; Mismatches 56;	QryMatch 41.8%; Indels 12; Gaps 10;
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Dbb	60	-L--V-YTIKQMYRGFSKMPHVQVYIHTAESESGLGLKLEVN-KYQVILITGRVY-EGKM 113
Qyy	65	PIKRIQIEIKRIQIMFTFG-PEK-DIEFIYTPASSAVCGVSLDVGGKGYLLIAGAEQDGKM 122
Dbb	114	YTGLENFVERWMDHLTISQKGLNRYRHLGCNCKIKSCYYLPCFTVSENECLWMDMLSNFG 173
Qyy	123	HITLCDIFVDPWDLTSTQKSLNHRVQMGCECKITRCPMIFCYISSEDECLMDWWTENK 182
Dbb	174	YPGYSKHXYACIRQKGYGYSWTRGNAPDPKSTSNATDP 211
Qyy	183	INGHQAKFFACIRSDGSCAWYRGAPPKQEFLDIEDP 220

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RESULT 11
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DT 01-JAN-1900
XX
DE Sequence 15, Application US/08134231.
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XX Sequence 15, Application US/08134231.
GENERAL INFORMATION:
CC APPLICANT: Silbiger, Scott M.
CC APPLICANT: Koski, Raymond A.
CC TITLE OF INVENTION: Tissue Inhibitor Metalloproteinase Type
CC TITLE OF INVENTION: Three Inhibitor Metalloproteinase Type
CC TITLE OF INVENTION: Three (TIMP-3) Composition and Methods
CC NUMBER OF SEQUENCES: 21
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Angen Inc./Patent Operations/KMP
CC STREET: 1840 Dehavilland Drive
CC CITY: Thousand Oaks
CC STATE: California
CC COUNTRY: USA
CC ZIP: 91320-1789
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/134,231
CC FILING DATE:
CC CLASSIFICATION: 424
CC INFORMATION FOR SEQ ID NO: 15:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 198 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC

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RESULT	12
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XX	STANDARD; PRT;
AC	xxxxxx
DT	01-JAN-1900
DE	Sequence 15, Application PC/TUS9411241.
XX	
CC	Sequence 15, Application PC/TUS9411241
CC	GENERAL INFORMATION:
CC	APPLICANT: Silbiger, Scott M.
CC	APPlicant: Koski, Raymond A.
CC	TITLE OF INVENTION: Tissue Inhibitor Metalloprotease
CC	TITLE OF INVENTION: Three (TIMP-3) Composition and Method of Use
CC	NUMBER OF SEQUENCES: 21
CC	CORRESPONDENCE ADDRESS:
CC	ADDRESSEE: Amgen Inc./Patent Operations/KMP
CC	STREET: 1840 Behavilland Drive
CC	CITY: Thousand Oaks
CC	STATE: California
CC	COUNTRY: USA
CC	ZIP: 91320-1789
CC	COMPUTER READABLE FORM:
CC	MEDIUM TYPE: Floppy disk
CC	COMPUTER: IBM PC compatible
CC	OPERATING SYSTEM: PC-DOS/MS-DOS
CC	SOFTWARE: PatentIn Release #1.0, Version #1.25
CC	CURRENT APPLICATION DATA:
CC	APPLICATION NUMBER: PCT/US94/11241
CC	FILING DATE:
CC	CLASSIFICATION:
CC	INFORMATION FOR SEQ ID NO: 15:
CC	SEQUENCE CHARACTERISTICS:
CC	LENGTH: 198 amino acids
CC	TYPE: amino acid
CC	STRANDNESS: single
CC	TOPOLOGY: linear

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XX	xxxxxx	
DT	01-JAN-1900	
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DE	Sequence 1, Application 05/08167463.	

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Sequence 1, Application US/08167463.
Sequence 1, Application US/08167463.
GENERAL INFORMATION:
APPLICANT: HAWKES, SUSAN P.
APPLICANT: KISHNANI, NARENDRA S
APPLICANT: YANG, TE-TUAN
TITLE OF INVENTION: HUMAN TIME-
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOURSTE
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-D
SOFTWARE: PatentIn Release #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/167
FILING DATE: 13-DEC-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 2200
TELECOMMUNICATION INFORMATION:

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RESULT	14
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STANDARD;	PRT; 164 AA.

XX	ID	US-08-134-231-17	STANDARD;
XX	AC	XXXXXX	
XX	DT	01-JAN-1900	
XX	DE	Sequence 17, Application US/08134231.	

Sequence 17, Application US/08134231.

Sequence 17, Application US/08134231

GENERAL INFORMATION:

APPLICANT: Silbiger, Scott M.

APPLICANT: Koski, Raymond A.

TITLE OF INVENTION: Tissue Inhibitor Metalloproteinase Type

TITLE OF INVENTION: Three (TIMP-3) Composition and Methods

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Amgen Inc./Patent Operations/KMP

STREET: 1840 Dehavilland Drive

City: Thousand Oaks

STATE: California

COUNTRY: USA

ZIP: 91320-1789

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/134,231
 CC FILING DATE:
 CC CLASSIFICATION: 424
 CC INFORMATION FOR SEQ ID NO: 17:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 164 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 164 AA; 19117 MW; 146524 CN;
 DB 30; Score 556; Match 41.8%; QryMatch 33.8%; Pred. No. 9,90e-48;
 Matches 66; Conservative 43; Mismatches 45; Indels 4; Gaps 4;
 Db 9 PFGTLVYTIKQMKMYRGFTKMPHVQYIHTAESLGLKLEVN-KYQYLLTGRVY-DGKM 66
 Qy 65 PIKRIQVEIKQIMFKG-PEK-DIEFIYAPSSAVGVSIDVGGKKEYLIAGKAEQDGM 122
 Db 67 YTGCLNFVERWDQLTISQKGLNRYHLGCNCKIKSCYILPCFVTSKNECLWMLNFG 126
 Qy 123 HITLCDPFIWPTLTSTQKSLNHRVYQMGCECKITRCMPICYSIDPECLMMDWVTEKN 182
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RESULT 15
 ID PCT-US94-11241-17 STANDARD; PRT; 164 AA.
 XX AC xxxxxx
 XX DT 01-JAN-1900
 XX DE Sequence 17, Application PC/TUS9411241.

Sequence 17, Application PC/TUS9411241
 GENERAL INFORMATION:
 CC APPLICANT: Silbiger, Scott M.
 CC APPLICANT: Koski, Raymond A.
 CC TITLE OF INVENTION: Tissue Inhibitor Metalloproteinase Type
 CC NUMBER OF SEQUENCES: 21
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Amgen Inc./Patent Operations/KMP
 CC STREET: 1840 Dehavilland Drive
 CC CITY: Thousand Oaks
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 91320-1789
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: PatentIn Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US94/11241
 CC FILING DATE:
 CC CLASSIFICATION:

CC INFORMATION FOR SEQ ID NO: 17:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 164 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 164 AA; 19117 MW; 146524 CN;
 DB 4; Score 556; Match 41.8%; QryMatch 33.8%; Pred. No. 9,90e-48;
 Matches 66; Conservative 43; Mismatches 45; Indels 4; Gaps 4;
 Db 9 PFGTLVYTIKQMKMYRGFTKMPHVQYIHTAESLGLKLEVN-KYQYLLTGRVY-DGKM 66
 Qy 65 PIKRIQVEIKQIMFKG-PEK-DIEFIYAPSSAVGVSIDVGGKKEYLIAGKAEQDGM 122
 Db 67 YTGCLNFVERWDQLTISQKGLNRYHLGCNCKIKSCYILPCFVTSKNECLWMLNFG 126
 Qy 123 HITLCDPFIWPTLTSTQKSLNHRVYQMGCECKITRCMPICYSIDPECLMMDWVTEKN 182
 Db 127 YPGYOSKHVACIRQKGGYCSWYRGWAPPDKSIINATDP 164
 Qy 183 INGHQAFACIKRSDGSCAWYGAAPPKQEFIDIEDP 220
 Search completed: Mon Feb 5 17:04:01 1996
 Job time : 118 secs.

 MARY HALE (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
 Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
 Distribution rights by IntelliGenetics, Inc.
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 Run on: Mon Feb 5 16:59:25 1996; MasPar time 11.53 Seconds
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 Description: (1:220) from trans.pap
 Perfect Score: 1643
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 Scoring table:
 PAM 150
 Gap 11
 Searched: 82306 seqs, 25270970 residues
 Database: pir46

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2 ann2
3 ann3
4 unann1
5 unann2
6 unann3
7 unann4
8 unann5
9 unann6
10 unann7
11 unann8
12 unrev1
13 unrev2

Statistics: Mean 42.711; Variance 87.125; scale 0.490

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1550	94.3	220	4 A35996	metalloproteinase in	1.14e-286
5	1466	89.2	196	4 S38624	metaro proteinase in	2.88e-269
6	1392	84.7	185	4 S21303	metalloproteinase in	5.84e-254
7	695	42.3	211	10 S45317	metalloproteinase ti	1.44e-111
8	686	41.8	212	10 A34329	metalloproteinase in	9.19e-110
9	686	41.8	211	11 A35332	tissue inhibitor of	9.19e-110
10	686	41.8	211	11 S43052	metalloproteinase-3	9.19e-110
11	680	41.4	210	10 S47041	mig protein - human	1.46e-108
12	677	41.2	198	11 S43053	metalloproteinase-3	5.82e-108
13	676	41.1	197	11 A49614	tissue inhibitor of	9.23e-108
14	521	31.7	207	2 ZYH0EP	metalloproteinase ti	5.23e-77
15	517	31.5	206	4 A33350	metalloproteinase in	2.03e-76
16	517	31.5	207	4 A35685	metalloproteinase in	3.19e-76
17	508	30.9	217	13 JC2557	metalloproteinase 1	1.86e-74
18	506	30.8	205	4 A26106	collagenase inhibito	4.57e-74
19	488	29.7	207	4 A26633	metalloproteinase in	1.51e-70
20	186	11.3	57	10 A39043	21K extracellular ma	1.56e-14
21	172	10.5	31	4 S18428	metalloproteinase in	3.20e-12
22	164	10.0	22	13 S20325	metalloproteinase in	6.35e-11
23	138	8.4	22	13 S20326	metalloproteinase in	7.42e-07
24	122	7.4	21	4 B39120	30K metalloproteinase	1.71e-04
25	117	7.1	290	7 S15198	hydrogenase isozyme	8.78e-04
26	100	6.1	76	11 S25146	CD24 protein - rat	1.74e-01
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28	98	6.0	1025	9 S42507	probable membrane pr	3.14e-01
29	96	5.8	141	13 S15785	heat-stable antigen	5.63e-01
30	96	5.8	76	13 S15784	heat-stable antigen	5.63e-01
31	96	5.8	76	11 S43709	heat-stable antigen	5.63e-01
32	96	5.8	76	11 A43537	heat-stable antigen	5.63e-01
33	96	5.8	76	11 S43529	heat-stable antigen	5.63e-01
34	93	5.7	310	10 S53717	dlk protein - human	1.33e+00
35	93	5.7	404	7 B45313	putrescine transport	1.33e+00

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38 91 5.5 3033 3 GNVJ18 genome polyprotein - 2.33e+00
39 90 5.5 806 6 A46271 integrin beta p, int 3.08e+00
40 90 5.5 26 4 A48417 gelatinase, 96K - hu 3.08e+00
41 90 5.5 805 6 A42483 integrin beta-7 chain 3.08e+00
42 90 5.5 806 6 B46503 beta 7 integrin=lymp 3.08e+00
43 89 5.4 361 11 A53860 chondroaderin precu 4.06e+00
44 89 5.4 1036 12 S55984 probable homeobox-do 4.06e+00
45 89 5.4 112 4 B24773 protein-tyrosine kin 4.06e+00

ALIGNMENTS

RESULT 1
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TITLE metalloproteinase tissue inhibitor 2 precursor - human
ORGANISM #formal name Homo sapiens #common name man
DATE 08-Mar-1991 #sequence_revision 08-Mar-1991 #text_change 05-Apr-1995
ACCESSIONS A37128; B35996; A34464; A34415
REFERENCE A37128
#authors Stetler-Stevenson, W.G.; Brown, P.D.; Onisto, M.; Levy, A.T.; Liotta, L.A.
#journal J. Biol. Chem. (1990) 265:13933-13938
#title Tissue inhibitor of metalloproteinases-2 (TIMP-2) mRNA expression in tumor cell lines and human tumor tissues.
#cross-references MUID:90338014
#accession A37128
#molecule_type mRNA
#residues 1-220 #label STE
#cross-references GB:J05593
REFERENCE A35996
#authors Boone, T.C.; Johnson, M.J.; De Clerck, Y.A.; Langley, K.E.
#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:2800-2804
#title cDNA cloning and expression of a metalloproteinase inhibitor related to tissue inhibitor of metalloproteinases.
#cross-references MUID:90207285
#accession B35996
#molecule_type mRNA
#residues 1-220 #label BOO
#cross-references GB:M32304
REFERENCE A34464
#authors Stetler-Stevenson, W.G.; Kruttsch, H.C.; Liotta, L.A.
#journal J. Biol. Chem. (1989) 264:17374-17378
#title Tissue inhibitor of metalloproteinase (TIMP-2). A new member of the metalloproteinase inhibitor family.
#cross-references MUID:90008902
#accession A34464
#molecule_type protein
#residues 27-77, 'K', '79-81, 'I', '83-100, 'E', '102-117, '119-121, 'R', '123-149, 'Q', '151-174, 'T', '176-219 #label ST2
REFERENCE A34415
#authors Goldberg, G.I.; Marmer, B.L.; Grant, G.A.; Eisen, A.Z.; Wilhelm, S.; He, C.
#journal Proc. Natl. Acad. Sci. U.S.A. (1989) 86:8207-8211
#title Human 72-kilodalton type IV collagenase forms a complex with a tissue inhibitor of metalloproteinases designated TIMP-2.
#cross-references MUID:90046765
#accession A34415

```
##molecule_type protein
##residues 30-51;124-141;159-173 ##label GOL
GENETICS
#gene GDB:TIMP2
#map position 17q25
CLASSIFICATION #superfamily metalloproteinase inhibitor
KEYWORDS extracellular protein; proteinase inhibitor
FEATURE
1-26 #domain signal sequence #status experimental #label SIG\
27-220 #product metalloproteinase tissue inhibitor 2 #status
experimental #label MAT
SUMMARY #length 220 #molecular-weight 24399 #checksum 6096
DB 4; Score 1643; Match 100.0%; QryMatch 100.0%; Pred. No. 0.00e+00;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 mgaartlrlalglalllratllrpdadacscspvhpqgafcnadvirakavsekevdsgnd 60
|||||
Qy 1 MGAARTLRLALGLLLLATLLRPADACSCSPVHPQQAFCNADVVIRAKAVSEKEVDSGND 60
|||||
Db 61 iynpikriqyeikqkfmfkgpkdiefiytapssavcgvslvvggkkeyliagkaegdg 120
|||||
Qy 61 IYGNPIKRIQYEIKQKFMFGPEKDIEFIYTAPSSAVCGVSLDVGGKKEYLIAGKAEGDG 120
|||||
Db 121 kmhitlcdfivpwtlstaqtkslnhrygmqgcekitrcpmipcyispsdeclmwdwvte 180
|||||
Qy 121 KMHITLCDFIVPWTLSLTQKSLNHRYPQMGECKITRCPMIPCYISPSDECLMWDWVTE 180
|||||
Db 181 kninghqakffacikrdsqscawrgaapkpqgefildiedp 220
|||||
Qy 181 KNINGHQAKFFACIKRDSGSCAWYRGAAAPPKQEFLDIEDP 220
|||||
RESULT 2
ENTRY #type complete
TITLE metalloproteinases-2 -- rat
ORGANISM #formal name Rattus norvegicus #common name Norway rat
DATE 10-Dec-1994 #sequence_revision 10-Dec-1994 #text_change
10-Dec-1994
ACCESSIONS S45683
REFERENCE #authors Cook, T.F.; Burke, J.S.; Bergman, K.D.; Quinn, C.O.; Jeffrey,
J.J.; Partridge, N.C.
#journal Arch. Biochem. Biophys. (1994) 311:313-320
#title Cloning and regulation of rat tissue inhibitor of
metalloproteinases-2 in osteoblastic cells.
#accession S45683
#status preliminary
##residues 1-220 ##label COO
SUMMARY #length 220 #molecular-weight 24369 #checksum 6329
DB 13; Score 1630; Match 98.2%; QryMatch 99.2%; Pred. No. 2.89e-303;
Matches 216; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Db 1 mgaartlrlalglalllratllrpdadacscspvhpqgafcnadvirakavsekevdsgnd 60
|||||
Qy 1 MGAARTLRLALGLLLLATLLRPADACSCSPVHPQQAFCNADVVIRAKAVSEKEVDSGND 60
|||||
Db 61 iynpikriqyeikqkfmfkgpkdiefiytapssavcgvslvvggkkeyliagkaegdg 120
|||||
```

```
Qy 61 IYGNPIKRIQYEIKQKFMFGPEKDIEFIYTAPSSAVCGVSLDVGGKKEYLIAGKAEGDG 120
|||||
Db 121 kmhitlcdfivpwtlstaqtkslnhrygmqgcekitrcpmipcyispsdeclmwdwvte 180
|||||
Qy 121 KMHITLCDFIVPWTLSLTQKSLNHRYPQMGECKITRCPMIPCYISPSDECLMWDWVTE 180
|||||
Db 181 ksqinghqakffacikrdsqscawrgaapkpqgefildiedp 220
|||||
Qy 181 KNINGHQAKFFACIKRDSGSCAWYRGAAAPPKQEFLDIEDP 220
|||||
RESULT 3
ENTRY #type complete
TITLE metalloproteinase inhibitor 2 precursor, tissue - mouse
ORGANISM #formal name Mus musculus #common name house mouse
DATE 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
28-Apr-1995
ACCESSIONS JH0683; JCI234; S26189
REFERENCE #authors Shimizu, S.; Malik, K.; Sejima, H.; Kishi, J.; Hayakawa, T.;
Koizumi, O.
#journal Gene (1992) 114:291-292
#title Cloning and sequencing of the cDNA encoding a mouse tissue
inhibitor of metalloproteinase-2.
#cross-references MUID:92290292
#accession JH0683
##molecule_type mRNA
##residues 1-220 ##label SHI
##cross-references EMBL:X62622
##experimental source 3T3 fibroblast, strain Balb/c
REFERENCE JCI234
#authors Leco, K.J.; Hayden, L.J.; Sharma, R.R.; Rocheleau, H.;
Greenberg, A.H.; Edwards, D.R.
#journal Gene (1992) 117:209-217
#title Differential regulation of TIMP-1 and TIMP-2 mRNA expression
in normal and Ha-ras-transformed murine fibroblasts.
#cross-references MUID:92347695
#accession JCI234
##molecule_type mRNA
##residues 1-11,'H',13-20,'L',22-194,'E',196-220 ##label LEC
##cross-references GB:M93954
CLASSIFICATION #superfamily metalloproteinase inhibitor
KEYWORDS metalloproteinase inhibitor
FEATURE
1-26 #domain signal sequence #status predicted #label SIG\
27-220 #product metalloproteinase inhibitor 2, tissue #status
predicted #label MAT
SUMMARY #length 220 #molecular-weight 24328 #checksum 6045
DB 4; Score 1620; Match 97.3%; QryMatch 98.6%; Pred. No. 3.44e-301;
Matches 214; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
Db 1 mgaartlrlalglalllratllrpdadacscspvhpqgafcnadvirakavsekevdsgnd 60
|||||
Qy 1 MGAARTLRLALGLLLLATLLRPADACSCSPVHPQQAFCNADVVIRAKAVSEKEVDSGND 60
|||||
Db 61 iynpikriqyeikqkfmfkgpkdiefiytapssavcgvslvvggkkeyliagkaegdg 120
|||||
Qy 61 IYGNPIKRIQYEIKQKFMFGPEKDIEFIYTAPSSAVCGVSLDVGGKKEYLIAGKAEGDG 120
|||||
```

Db 121 kmhltcdfiwpdwtlstkkslnhrygmgeckitrcpmipcyispsdeclwmdwvte 180
Qy 121 kmhltcdfiwpdwtlstkkslnhrygmgeckitrcpmipcyispsdeclwmdwvte 180
Db 181 kslngqakffacikrsdgscaawyrgaappkqefldiedp 220
Qy 181 kslngqakffacikrsdgscaawyrgaappkqefldiedp 220

RESULT 4
ENTRY A35996 #type complete
TITLE metalloproteinase inhibitor 2 precursor - bovine
ALTERNATE_NAMES collagenase inhibitor; tissue inhibitor of metalloproteinases (TIMP-2)
ORGANISM #formal name Bos primigenius taurus #common name cattle
DATE 16-Nov-1990 #sequence_revision 16-Nov-1990 #text_change 05-Apr-1995
ACCESSIONS A35996; A34468; A25322; S28151
REFERENCE A35996
#authors Boone, T.C.; Johnson, M.J.; De Clerck, Y.A.; Langley, K.E.
#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:2800-2804
#title cDNA cloning and expression of a metalloproteinase inhibitor related to tissue inhibitor of metalloproteinases.
#cross-references MUID:90207285
#accession A35996
##molecule_type mRNA
##residues 1-220 #label BOO
##cross-references GB:M2303
##experimental_source aortic endothelium
REFERENCE A34468
#authors De Clerck, Y.A.; Yean, T.D.; Ratzkin, B.J.; Lu, H.S.; Langley, K.E.
#journal J. Biol. Chem. (1989) 264:17445-17453
#title Purification and characterization of two related but distinct metalloproteinase inhibitors secreted by bovine aortic endothelial cells.
#cross-references MUID:90008914
#accession A34468
##status preliminary
##molecule_type protein
##residues 27-71 #label DEC
REFERENCE A25322
#authors Murray, J.B.; Allison, K.; Sudhalter, J.; Langer, R.
#journal J. Biol. Chem. (1986) 261:4154-4159
#title Purification and partial amino acid sequence of a bovine cartilage-derived collagenase inhibitor.
#cross-references MUID:86140235
#accession A25322
##molecule_type protein
##residues 27-41, 'C', '43-55', 'EX', '58-59', 'X', '61-66', 'XS', '69-71' #label MTR
##experimental_source cartilage
REFERENCE S28151
#authors DeClerck, Y.A.; Yean, T.D.; Lee, Y.; Tomich, J.M.; Langley, K.E.
#journal Biochem. J. (1993) 289:65-69
#title Characterization of the functional domain of tissue inhibitor of metalloproteinases-2 (TIMP-2).
#contents annotation; functional domain
CLASSIFICATION #superfamily metalloproteinase inhibitor

KEYWORDS proteinase inhibitor
FEATURE #domain signal sequence #status predicted #label SIG\
1-26 #product metalloproteinase inhibitor 2 #status predicted
27-220 #label MAT\
27-158 #region inhibitory #status predicted
SUMMARY #length 220 #molecular-weight 24355 #checksum 3345

DB 4; Score 1550; Match 91.8%; QryMatch 94.3%; Pred. No. 1.14e-286; Matches 202; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

Db 1 mqaarslplafcllltllptadacspvhpqqafcnadivirakavnkkevdsdgn 60
Qy 1 mqaarturlalglalltlrpadacsfvhpqqafcnadivirakavsekevdsdgn 60
Db 61 iypnpikriqveikmfgkpdgdiefiytapaavcgvaldiggtkeyliagkaesg 120
Qy 61 iypnpikriqveikmfgkpekdiefiytapsavcgvaldiggtkeyliagkaesg 120
Db 121 nmhltcdfiwpdwtlstkkslnhrygmgeckitrcpmipcyispsdeclwmdwvte 180
Qy 121 kmhltcdfiwpdwtlstkkslnhrygmgeckitrcpmipcyispsdeclwmdwvte 180
Db 181 kninghqakffacikrsdgscaawyrgaappkqefldiedp 220
Qy 181 kninghqakffacikrsdgscaawyrgaappkqefldiedp 220

RESULT 5
ENTRY S38624 #type fragment
TITLE metaro proteinase inhibitor, tissue - Chinese hamster (fragment)
ORGANISM #formal name Cricetulus griseus #common name Chinese hamster
DATE 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 12-Apr-1995
ACCESSIONS S38624
REFERENCE S38624
#authors Suzuki, Y.
#submission submitted to the EMBL Data Library, November 1993
#accession S38624
##status preliminary
##molecule_type mRNA
##residues 1-196 #label S02
##cross-references EMBL:X75924
CLASSIFICATION #superfamily metalloproteinase inhibitor
SUMMARY #length 196 #checksum 7766

DB 4; Score 1466; Match 99.0%; QryMatch 89.2%; Pred. No. 2.88e-269; Matches 193; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 2 acscspvhpqgafcnadivirakavsekevdsdgnidvgnpikriqveikmfgkpdkd 61
Qy 26 acscspvhpqgafcnadivirakavsekevdsdgnidvgnpikriqveikmfgkpekd 85
Db 62 lefiytpassavcgvaldiggtkeyliagkaesgdkmhltcdfiwpdwtlstkksln 121
Qy 86 lefiytpassavcgvaldiggtkeyliagkaesgdkmhltcdfiwpdwtlstkksln 145
Db 122 hrygmgeckitrcpmipcyispsdeclwmdwvteknghqakffacikrsdgscaawy 191


```
QY 146 HRYOMGECKITRCMPICVYISSPDECLWMDVWTEKNGHOAKFCIKRSDGSCAWYR 205
Db 182 gaappkqefldiedp 196
QY 206 GAAPKQEFLDIEDP 220

RESULT 6 S21303 #type fragment
ENTRY metalloproteinase inhibitor 2, tissue - human (fragment)
TITLE #formal name Homo sapiens #common name man
ORGANISM 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
DATE 12-Apr-1995

ACCESSIONS S21303
REFERENCE S21303
#authors Malik, K.; Sejima, H.; Aoki, T.; Iwata, K.
#submission submitted to the EMBL Data Library, August 1990
#description Nucleotide sequence of a TIMP-II cDNA.
#accession S21303

##status preliminary
##molecule_type mRNA
##residues 1-185 #label MAL
##cross-references EMBL:X54533
CLASSIFICATION #superfamily metalloproteinase inhibitor
SUMMARY #length 185 #checksum 2530

Db 4; Score 1392; Match 99.5%; QryMatch 84.7%; Pred. No. 5.84e-254;
Matches 184; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 spvhpqafcnadvirakavsekevdsgndiynpikriyveikqikmfkgpekdiefi 60
QY 30 SPVHPQAFCNADVIRAKAVSEKEVDSGNDIYNPIKRIYVEIKQIKMFKGPEKDIEFI 89

Db 61 ytapssvvcgvsldvggkkeyliagkaeqdgknhitlcdfivpwtltatgkkslnhryq 120
QY 90 YTAPSSAVCGVSLDVGKKEYLIAGKAEDGKMHITLCDFIVPWTLTSTTQKKSINHRYQ 149

Db 121 mgceckitrcpmipcyisspdeclwmdvteknghqakffacikrdsdcawyr gaap 180
QY 150 MGCECKITRCMPICVYISSPDECLWMDVTEKNNGHOAKFFACIKRSDGSCAWYRGAAP 209

Db 181 pkqef 185
QY 210 PKQEF 214

RESULT 7 S45317 #type complete
ENTRY metalloproteinase tissue inhibitor 3 - human
TITLE #formal name Homo sapiens #common name man
ORGANISM 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
DATE 03-Mar-1995

ACCESSIONS S45317
REFERENCE S45317
#authors Uria, J.A.; Ferrando, A.A.; Velasco, G.; Freije, J.M.P.;
#journal Lopez-Otin, C.
#title Cancer Res. (1994) 54:2091-2094
#accession S45317
Structure and expression in breast tumors of human TIMP-3, a
new member of the metalloproteinase inhibitor family.
```

```
##status preliminary
##molecule_type mRNA
##residues 1-211 #label URI
##cross-references EMBL:X76227
SUMMARY #length 211 #molecular-weight 24145 #checksum 4550

Db 10; Score 695; Match 43.6%; QryMatch 42.3%; Pred. No. 1.44e-111;
Matches 95; Conservative 56; Mismatches 55; Indels 12; Gaps 10;

Db 2 tpwlgilvlgswlsgdgaectspshpdaefcnsvdivirakvvgkklvkegp---fgt 59
QY 7 TIRLALGULLLA-TLL-RPADACSCSEVHPQAFCNADVIRAKAVSEKEVDSCNDIYGN 64

Db 60 l--v-ytikmqmrygrftkmpvhyihteaeslqgkllevn-kyqyllitgrvy-dgkm 113
QY 65 PIKRIQYEIKQIKMFKG--PEK-DIEFIYAPSSAVCGVSLDVGKKEYLIAGKAEDGDKM 122

Db 114 ytgicnfverwdqitlsqrkglvnyrhlgcncikskicyllpcfvtskneclwdmlsnfg 173
QY 123 HITLCLDFIVPWTLTSTTQKKSINHRYOMGECKITRCMPICVYISSPDECLWMDVWTEKN 182

Db 174 ypgyqskhyacirqkgycswyrgwappdkssiinatdp 211
QY 183 INGHQAKFFACIKRSDGSCAWYRGAAPKQEFLDIEDP 220

RESULT 8 A43429 #type complete
ENTRY metalloproteinase inhibitor CHIMP-3 - chicken
TITLE #formal name Gallus gallus #common name chicken
ORGANISM 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change
DATE 11-Apr-1995

ACCESSIONS A43429
REFERENCE A43429
#authors Pavloff, N.; Staskus, P.W.; Kishnani, N.S.; Hawkes, S.P.
#journal J. Biol. Chem. (1992) 267:17321-17326
#title A new inhibitor of metalloproteinases from chicken: CHIMP-3.
#cross-references MIM:92381050
#accession A43429

##status preliminary
##molecule_type mRNA
##residues 1-212 #label PAV
##cross-references NCBI:111960; NCBI:111961
##experimental_source embryo
##note #sequence extracted from NCBI backbone
SUMMARY #length 212 #molecular-weight 24504 #checksum 6267

Db 10; Score 686; Match 45.2%; QryMatch 41.8%; Pred. No. 9.19e-110;
Matches 90; Conservative 49; Mismatches 50; Indels 10; Gaps 8;

Db 22 aeactcvpibpqdafcnsvdivirakvvgkklmkdgp---fgt-m-r--ytvqkmkmyrgfq 75
QY 24 ADACSCSEVHPQAFCNADVIRAKAVSEKEVDSCNDIYGNPIKRIQYEIKQIKMFKG-P 82

Db 76 imphvqvlyiteaseslqgklevn-kyqyllitgrvy-egkvtyglcnwyekwdriltlsqr 133
QY 83 EK-DIEFIYAPSSAVCGVSLDVGKKEYLIAGKAEDGKMHITLCLDFIVPWTLTSTQK 141

Db 134 kglhryhlgcgckirpcyylpcfateknciwtmnlsgnfhghsqhqdahyaciqrvegyc 193
```

Qv 142 KSLNHRYOMGCEKTRCPMPICVYSSPDECLMWDWTEKNINGHOAKFFACIKRSDGSC 201

```

Db 194 swyrgwappdktiinatdp 212
    :|||||:::
Qv 202 AWYRGAAPPKQEFFLDIEDP 220

```

```

RESULT      9
ENTRY       A53532      #type complete
TITLE       tissue inhibitor of metalloproteinases-3 - mouse
            ALTERNATE_NAMES
ORGANISM_NAMES
DATE        27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change
            27-Jun-1994
ACCESSIONS  A53532
REFERENCE   Leco, K.J.; Khokha, R.; Pavloff, N.; Hawkes, S.P.; Edwards,
            D.R.
            J. Biol. Chem. (1994) 269:9352-9360
            Tissue inhibitor of metalloproteinases-3 (TIMP-3) is an
            extracellular matrix-associated protein with a distinctive
            pattern of expression in mouse cells and tissues.
            #accession  A53532
            #status     preliminary
            #molecule_type  mRNA
            #residues    1-211  #label  LEC
            #cross-references  GB:L27424

```

m	TIMP-3	#length	211	#molecular-weight	24182	#checksum	4940
SUMMARY							
#gene							

DB 11;	Score	686;	Match	43.1%;	QryMatch	41.8%;	Pred.	No.	9.19e-110;
Matches	94:	Conservative	56;	Mismatches	56;	Indels	12;	Gaps	10;

Db	2	tpwlglvllscswslghwdaeactspshpqdafcnsdivirakvvgkklvkegp--fgt	59
		: : : : : : : : : : : : : : : : : :	
		: : : : : : : : : : : : : : : : : :	
QV	7	TRIALGILLLA-TL-LRPADACSSPVHPQOAFCNADWIRAKVSEKVEDSGNDIYGN	64

Db 60 -l--v-ytikmqkmyrgfakmhpvcyihtheaseslgcllevn-kyqylltgrvy-egkm 113
: llll::l: : :: l: :ll: l: |::l: :|l:
QV 65 PIKRIQVEIKOIKMFKG-PEK-DIEFIYTPSSAVCGVSLDVGKGKEYLIAGKAEGDKM 122

```

114 ytglnfverwdhtlsqrkglnryvhlgcncikksyylpcfvtskneclwtmdlsmfng 173
      |||: || |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |:
123 HITLCPFLVPWDLSTQKKSLSNHRVOMGCSEKITRCMPICVYSSPDECLMWDWTEKN 182

```

```
Db      174 ypgvqskhyacirqkkgycswyrgwappdkksisnatdp 211  
          _|_| :|||:: |_|:||| ||| : |  
QV     183 INGHAKFFACIKRSDGSCAWYRGAAPKKOEFLDIEDP 220
```

RESULT	10
ENTRY	S43052
TITLE	#type complete
ORGANISM	metalloproteinase-3 tissue inhibitor - mouse
DATE	#formal name Mus musculus #common name house mouse
	06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
ACCESSIONS	06-Jan-1995
REFERENCE	S43052

```
#authors      Sun, Y.
#submission   submitted to the EMBL Data Library, March 1994
#accession    S43052
```

```
##molecule_type DNA
##residues 1-211 ##label SUN
##cross-references EMBL:Z30970
##length 211 ##molecular_weight 211
```

#cross-references	EMBL.250570
#length	211
#molecular-weight	24182
#checksum	4940
SUMMARY	

DB 11; Score 686; Match 43.1%; QryMatch 41.8%; Pred. No. 9.19e-110;	
Matches 94; Conservative 56; Mismatches 56; Indels 12; Gaps 10;	

Db 2 tptwlgvllscwslghwgaeactcspshpqdafncsdvirakvvgkklvkpg--fgt 59
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QV 7 TTELALGLLLA-TI-LRPDADACSCSEVHPQQAFCNADVIRAKAVSEKEVDSGNDIYN 64

Db 60 -l--v-ytikmqmrygfskmpbhvyihtheaseslclglevn-kyqylltgrvy-egkm 113
: | |||:|::: : :: | : |:|: | : |:|:|: :||
Qv 65 PIKRIQVEIKQIRMFKG-PEK-DIEFIYTPSSAVCGVSLDVGCKKEYLIAGKAEGDGKM 122

```
Db      114 ytglnfverwdhtlsqrkglnryvhlgenckikscvyllpcfvtskneclwtamlanf 173
        |||:: || |::||| |||::||| |::|||::||| |::|||::||| |::|||::|||
Qv      123 HITLDFVLPWDTLSTTKKSLNHRHYOMGECKITRGPMPICVISSPDECLMWDOWTEKN 182
```

```
Db      174 ypgyqskhyacirqkggygcswyrwgwapdpksisnatdp 211  
        _|| :| :|| :: -|| :|||| ||| : : ||  
Qv     183 INGHQAKFFACIKRSDGSCAWYRGGAAPPKOEFLDIEDP 220
```

RESULT	11
ENTRY	S47041
TITLE	m1g protein - human
ORGANISM	#formal name Homo sapiens
DATE	20-Feb-1995
	#sequence_rev 20-Feb-1995

SESSIONS
REFERENCE
#authors
S47041
S47041
Wick, M.; Buerger, C.; Brueselbach, S.; Lucibello, F.;
Mueller, R.

#submission submitted to the EMBL Data Library, February 1994
#description A novel member of the TTP gene family is regulated during G1 progression, mitogenic stimulation, differentiation and senescence.

```
#accession      S47041
##status        preliminary
##molecule_type DNA
##residues      1-210
##label         WIC
##cross-references EMBL:230183
```

#CROSS-REFERENCES	EMBL:Z50183
#length	210
#molecular-weight	24066
#checksum	2608
SUMMARY	

DB 10; Score 680; Match 43.5%; QryMatch 41.4%; Pred. No. 1.46e-108; Matches 93; Conservative 54; Mismatches 54; Indels 13; Gaps 10;

Db 5 lglvllgswsgwtgaprctcspshqdafcnstdivirakvvgkklvkpg--fgt-l-- 59
|||:: : | :||| |||::|||::|||::|||::|||::|||::|||::|||::
Qv 12 LGLL-LIATLLRPADA--CSCSPVHPDAAFNCADWITRAKAVSEKEVDSGNDYGNPKR 68

Db 60 v-ytiqmkmyrgftkmpbhvqihteaseslcgklievn-kyqvlltgrvy-dgkmytgI 116
 : | ||| :||| : :||| : :||| :| : :||| :| :||| :| :||| :| :||| :| :||| :
Qv 69 IOYEIKOIKMFKG-PEK-DIEFIYAPSSAVCGVSLDVGGKEYLIAGKAEGDGKMHTL 126


```
#accession A93363
##molecule_type mRNA
##residues 1-207 ##label GAS
REFERENCE A23534
#authors Carmichael, D.F.; Sommer, A.; Thompson, R.C.; Anderson, D.C.;
Smith, C.G.; Welgus, H.G.; Stricklin, G.P.
#journal Proc. Natl. Acad. Sci. U.S.A. (1986) 83:2407-2411
#title Primary structure and cDNA cloning of human fibroblast
collagenase inhibitor.
#cross-references M01D:86205964
#accession A23534
##molecule_type mRNA
##residues 1-207 ##label CAR
##note parts of this sequence were confirmed by protein
sequencing
##note carbohydrate binding sites were determined
REFERENCE A20595
#authors Stricklin, G.P.; Welgus, H.G.
#journal J. Biol. Chem. (1983) 258:12252-12258
#title Human skin fibroblast collagenase inhibitor.
#cross-references M01D:84032401
#accession A20595
##molecule_type protein
##residues 24-44, 'L', 46 ##label STR
##note six disulfide bonds are present
REFERENCE A35826
#authors Rapp, G.; Freudenstein, J.; Klaudiny, J.; Mucha, J.; Wempe,
F.; Zimmer, M.; Scheit, K.H.
#journal DNA Cell Biol. (1990) 9:479-485
#title Characterization of three abundant mRNAs from human ovarian
granulosa cells.
#cross-references M01D:91025550
#accession A35826
##molecule_type mRNA
##residues 1-207 ##label RAP
##cross-references GB:M38188
COMMENT This protein, found in a variety of body fluids, complexes with
metalloproteinases, irreversibly inactivating them. It also
mediates erythropoiesis in vitro; but, unlike IL-3, it is
species-specific, stimulating the growth and differentiation of
only human and murine erythroid progenitors.
COMMENT The remarkable heat stability of this protein may be due to
disulfide bond formation.
GENETICS
#gene GDB:TIMP1; CLGI; TIMP
#map position Xp11.3-p11.23
CLASSIFICATION #superfamily metalloproteinase inhibitor
KEYWORDS erythropoiesis; glycoprotein; proteinase inhibitor
FEATURE
1-23 #domain signal sequence #status predicted #label SIG\
24-207 #product metalloproteinase inhibitor #status predicted
#label MAT\
53,101 #binding_site carbohydrate (Asn) (covalent) #status
experimental
SUMMARY #length 207 #molecular-weight 23171 #checksum 9750
DB 2; Score 521; Match 41.1%; QryMatch 31.7%; Pred. No. 5.23e-77;
Matches 81; Conservative 39; Mismatches 70; Indels 7; Gaps 7;
Db 7 laegllllwliapsractcvpphqtacnsdlvirakfvgtpevngtt-lygryeikm 65
```

```
10 LAIGLLLLATLLRPADACSCSPVHPQQAFCNADVVIRAKAVSEKVDVSGNDIYGN-PIKR 68
66 tk-mvkgfql-gdaadirfvytpamesvcgyfhrshnrseefliagklq-dgllhitc 122
69 IQYEIKQIKMFKGPEKIDIEFIYTAPSSAVCGVSLDVGGKKE-YLIAGKAECDGKMHTLC 127
Db 123 sfvvpwnslsfqrgftktyvqceestvpfclspicklqsgthclwtcdqlllgaeqkf 182
Qy 128 DFIVPWTLSLTQKRSINHRVQMGCE--CKITRCMPICPIYSSDPDECLMWDVTEKNGH 186
Db 183 qsrhlacplrepdgtw 199
Qy 187 QAKFFACIKRSDGSCAW 203
RESULT 15
ENTRY A33350 #type complete
TITLE metalloproteinase inhibitor - rabbit
ORGANISM #formal_name Oryctolagus cuniculus #common_name domestic
rabbit
DATE 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
18-Jun-1993
ACCESSIONS A33350; A30864
REFERENCE A33350
#authors Horowitz, S.; Dafni, N.; Shapiro, D.L.; Holm, B.A.; Notter,
R.H.; Quiblie, D.J.
#journal J. Biol. Chem. (1989) 264:7092-7095
#title Hyperoxic exposure alters gene expression in the lung.
Induction of the tissue inhibitor of metalloproteinases
mRNA and other mRNAs.
#cross-references M01D:89214135
#accession A33350
##molecule_type mRNA
##residues 1-206 ##label HOR
##cross-references GB:J04712
COMMENT Expression of this protein in the lung is induced 6-fold by
hyperoxia.
CLASSIFICATION #superfamily metalloproteinase inhibitor
SUMMARY #length 206 #molecular-weight 22758 #checksum 4434
DB 4; Score 518; Match 40.1%; QryMatch 31.5%; Pred. No. 2.03e-76;
Matches 79; Conservative 39; Mismatches 71; Indels 8; Gaps 8;
Db 7 laegllllwliapsractcvpphqtacnsdlvirakfvgapenvhntt-lygryeik 65
10 LAIGLLLLATLLRPADACSCSPVHPQQAFCNADVVIRAKAVSEKVDVSGNDIYGN-PIKR 68
66 tk-mvkgfql-gdaadirfvytpamesvcgyfhrshnrseefliagklq-ngllhitc 122
69 IQYEIKQIKMFKGPEKIDIEFIYTAPSSAVCGVSLDVGGKKE-YLIAGKAECDGKMHTLC 127
Db 123 sfvvpwnslsfqrgftktyaagcdmctvfacasichesdthclwtddslgsd-kgf 181
Qy 128 DFIVPWTLSLTQKRSINHRVQMGCE--CKITRCMPICPIYSSDPDECLMWDVTEKNGH 186
Db 182 qsrhlacplrepdgtw 198
Qy 187 QAKFFACIKRSDGSCAW 203
```

Search completed: Mon Feb 5 17:00:15 1996
Job time : 50 secs.

M P S R H
***** (TM)

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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Mon Feb 5 17:00:33 1996; MasPar time 6.00 Seconds
Tabular output not generated. 562.012 Million cell updates/sec

Title: >FIG2
Description: (1:220) from trans.pep
Perfect Score: 1643
Sequence: 1 MGAARTLRALGILLATL.....CAWYGAAPPKQEFLLIEDP 220

Scoring table: PAM 150
Gap 11

Searched: 43470 seqs, 15335248 residues

Database: swiss-prot31
1 part1
2 part2
3 part3
4 part4
5 part5
6 part6
7 part7
8 part8

Statistics: Mean 44.257; Variance 69.417; scale 0.638

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1643	100.0	220	7	TIM2_HUMAN METALLOPROTEINASE INH	0.00e+00
2	1620	98.6	220	7	TIM2_MOUSE METALLOPROTEINASE INH	0.00e+00
3	1550	94.3	220	7	TIM2_BOVIN METALLOPROTEINASE INH	0.00e+00
4	695	42.3	211	7	TIM3_HUMAN METALLOPROTEINASE INH	8.10e-145

5	686	41.8	211	7	TIM3_MOUSE	METALLOPROTEINASE INH	1.77e-142
6	686	41.8	212	7	TIM3_CHICK	METALLOPROTEINASE INH	1.77e-142
7	521	31.7	207	7	TIM1_HUMAN	METALLOPROTEINASE INH	4.90e-100
8	518	31.5	206	7	TIM1_RABIT	METALLOPROTEINASE INH	2.84e-99
9	517	31.5	207	7	TIM1_BOVIN	METALLOPROTEINASE INH	5.09e-99
10	506	30.8	205	7	TIM1_MOUSE	METALLOPROTEINASE INH	3.16e-96
11	491	29.9	207	7	TIM1_PIG	METALLOPROTEINASE INH	1.99e-92
12	164	10.0	22	7	TIM2_RAT	METALLOPROTEINASE INH	9.30e-15
13	138	8.4	22	7	TIM1_RAT	METALLOPROTEINASE INH	1.43e-09
14	117	7.1	290	4	HYPB_ECOLI	HYDROGENASE ISOENZYME	1.13e-05
15	98	6.0	1025	8	YED7_YEAST	ALPHA-ADAPTIN HOMOLOG	1.85e-02
16	96	5.8	144	8	X62_MOUSE	X62 HEAT STABLE ANTIG	3.84e-02
17	96	5.7	76	4	M163_MOUSE	M1/69-J11D HEAT STABL	3.84e-02
18	93	5.7	404	6	POTG_ECOLI	PUTRESCINE TRANSPORT	1.12e-01
19	91	5.5	206	3	GPBB_HUMAN	PLATELET GLYCOPROTEIN	2.26e-01
20	91	5.5	3033	6	POLG_HCVJ8	GENOME POLYPROTEIN (C	2.26e-01
21	90	5.5	806	4	ITB7_MOUSE	INTEGRIN BETA-7 SUBUN	3.19e-01
22	89	5.4	1130	4	KABL_HUMAN	PROTO-ONCOGENE TYROSI	4.50e-01
23	89	5.4	1123	4	KABL_MOUSE	PROTO-ONCOGENE TYROSI	4.50e-01
24	88	5.4	80	2	CD24_HUMAN	SIGNAL TRANSDUCER CD2	6.32e-01
25	88	5.4	367	2	DIAC_RAT	DI-N-ACETYLCHITINBIASE	6.32e-01
26	85	5.2	428	5	NODC_RHILP	MODULATION PROTEIN C	1.72e+00
27	84	5.1	1058	6	POL3_DROME	RETROVIRUS-RELATED PO	2.38e+00
28	84	5.1	1042	2	EF3_FNECA	ELONGATION FACTOR 3 (2.38e+00
29	84	5.1	628	3	GIDA_BACSU	GLUCOSE INHIBITED DIV	2.38e+00
30	83	5.1	267	8	YATR_BACFI	HYPOTHETICAL ATP-BIND	3.28e+00
31	82	5.0	235	1	ATTE_HYACE	PROATTACIN E AND F PR	4.51e+00
32	82	5.0	671	2	COAT_FCVF9	COAT PROTEIN (CAPSID	4.51e+00
33	82	5.0	439	4	KABL_FSVHY	TYROSINE-PROTEIN KINA	4.51e+00
34	82	5.0	1013	6	POL_HUMAN	NAD(+) ADP-RIBOSYLTRA	4.51e+00
35	81	4.9	2116	5	MY52_DICDI	MYOSIN II HEAVY CHAIN	6.19e+00
36	81	4.9	971	4	MCW3_YEAST	MINICHROMOSOME MAINT	6.19e+00
37	81	4.9	399	2	DNAJ_STRCO	DNAJ PROTEIN.	6.19e+00
38	81	4.9	431	3	HISX_LACIA	HISTIDINOL DEHYDROGEN	6.19e+00
39	81	4.9	3010	6	POLG_HCVTW	GENOME POLYPROTEIN (C	6.19e+00
40	81	4.9	898	6	RA54_YEAST	DNA REPAIR AND RECOMB	6.19e+00
41	80	4.9	619	8	YOL8_CAEEL	HYPOTHETICAL 71.0 KD	8.45e+00
42	80	4.9	544	8	YB73_YEAST	HYPOTHETICAL 62.3 KD	8.45e+00
43	80	4.9	1015	6	PPOL_BOVIN	NAD(+) ADP-RIBOSYLTRA	8.45e+00
44	80	4.9	2265	3	FINC_BOVIN	FIBRONECTIN (FN).	8.45e+00
45	80	4.9	174	3	HDCB_LACS3	20 KD PROTEIN.	8.45e+00

ALIGNMENTS

RESULT	1	TIM2_HUMAN	STANDARD;	PRT;	220 AA.
ID	P16035,				
AC	01-APR-1990 (REL. 14, CREATED)				
DT	01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)				
DT	01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)				
DE	METALLOPROTEINASE INHIBITOR 2 PRECURSOR (TIMP-2) (TISSUE INHIBITOR OF TIMP2).				
GN	HOMO SAPIENS (HUMAN).				
OS	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC	EUTHERIA; PRIMATES.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RM	90338014				

RA STETTLER-STEVENSON W.G., BROWN P.D., ONISTO M., LEVY A.T., LIOTTA L.A.;
RL J. BIOL. CHEM. 265:13933-13938(1990).
RN [2]
RP SEQUENCE FROM N.A.
RM 90207285
RA BOONE T.C., JOHNSON M.J., DE CLERCK Y.A., LANGLEY K.E.;
RL PROC. NATL. ACAD. SCI. U.S.A. 87:2800-2804(1990).
RN [3]
RP SEQUENCE OF 30-214 FROM N.A.
RA MALIK K., SEJIMA H., AOKI T., IWATA K.;
RL SUBMITTED (AUG-1990) TO EMBL/GENBANK/DDJ DATA BANKS.
RN [4]
RP SEQUENCE OF 27-219.
RM 90009902
RA STETTLER-STEVENSON W.G., KRUTZSCH H.C., LIOTTA L.A.;
RL J. BIOL. CHEM. 264:17374-17378(1989).
RN [5]
RP SEQUENCE OF 30-51; 124-141 AND 159-173.
RM 90046765
RA GOLDBERG G.I., MARMER B.L., GRANT G.A., EISEN A.Z., WILHELM S., HE C.;
RL PROC. NATL. ACAD. SCI. U.S.A. 86:8207-8211(1989).
RN [6]
RP SEQUENCE OF 27-41.
RC TISSUE=SYNOVIAL FLUID;
RM 92111776
RA OSTHUES A., KNAUPER V., OBERHOFF R., REINKE H., TSCHESCHE H.;
RL FEBS LETT. 296:16-20(1992).
CC -1- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
CC AND IRREVERSIBLY INACTIVATE THEM.
CC -1- PTM: THE ACTIVITY OF TIMP-2 IS DEPENDENT ON THE PRESENCE OF
CC DISULFIDE BONDS.
CC -1- SIMILARITY: HIGH WITH OTHER MEMBERS OF THE TIMP FAMILY.
DR EMBL; J05593; HSTIMP2.
DR EMBL; M32304; HSMET.
DR EMBL; X54533; HSTIMP2M.
DR PIR; A34415; A34415.
DR PIR; A34464; A34464.
DR PIR; B35996; B35996.
DR PIR; A37128; A37128.
DR PIR; S20319; S20319.
DR MIM; 188825; 11TH EDITION.
DR PROSITE; PS00288; TIMP.
KW METALLOPROTEINASE INHIBITOR; SIGNAL.
FT SIGNAL 1 26
FT CHAIN 27 220 METALLOPROTEINASE INHIBITOR 2.
FT DISULFID 27 98 BY SIMILARITY.
FT DISULFID 29 127 BY SIMILARITY.
FT DISULFID 39 152 BY SIMILARITY.
FT DISULFID 154 201 BY SIMILARITY.
FT DISULFID 172 193 BY SIMILARITY.
FT DISULFID 159 164 BY SIMILARITY.
FT CONFLICT 78 78 M -> K (IN REF. 4).
FT CONFLICT 82 82 P -> I (IN REF. 4).
FT CONFLICT 96 96 A -> V (IN REF. 3).
FT CONFLICT 101 101 S -> E (IN REF. 4).
FT CONFLICT 118 118 MISSING (IN REF. 4).
FT CONFLICT 122 122 M -> R (IN REF. 4).
FT CONFLICT 150 150 M -> Q (IN REF. 4).
FT CONFLICT 175 175 M -> T (IN REF. 4).
SQ SEQUENCE 220 AA; 24399 MW; 242975 CN;

DB 7; Score 1643; Match 100.0%; OryMatch 100.0%; Pred. No. 0.00e+00;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 mgaartlrlalglalllratllrpdadacscspvhpqafcnadvvirakavsekevsgnd 60
Qy 1 MGAARTLRALGLALLLRLATLLRPADAGSCSPVHPQQAFCNADVVIRAKAVSEKEVDSGD 60
Db 61 iygnpikriqyeikqikmfkgpekdiefiytapssavcgvslvuggkkeyliagkaegdg 120
Qy 61 IYGNPIKRIQYEI KQIKMFKGPEKDIEFIY TAPSSAVCGVSLDVGGKKEYLIAGKAEGDG 120
Db 121 kmhitlclcfivpwtlslttgkkslnhryqmgceckitrcpmipcyisspdecilmwcdwvte 180
Qy 121 KMHITLCLCFIVPWTLSLTGKKS LNHR YQMGCECKITRCPMIPCYISSPDECLMWDVTE 180
Db 181 kninghqakfaccikrsdgcawyrsgaapkpqefldiedp 220
Qy 181 KNINGHQAKFACIKRSDGSCAWYRSGAAPKPQEFLDIEDP 220
RESULT 2
ID TIM2 MOUSE STANDARD; PRT; 220 AA.
AC P25785;
DT 01-MAY-1992 (REL. 22, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE METALLOPROTEINASE INHIBITOR 2 PRECURSOR (TIMP-2) (TISSUE INHIBITOR OF
DE METALLOPROTEINASES-2).
GN TIMP-2.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RM 92290292
RA SHIMIZU S., MALIK K., SEJIMA H., KISHI J.I., HAYAKAWA T., KOIWA O.;
RL GENE 114:291-292(1992).
RN [2]
RP SEQUENCE FROM N.A.
RM 92347695
RA LECO K.J., HAYDEN L.J., SHARMA R.R., ROCHELEAU H., GREENBERG A.H.,
RA EDWARDS D.R.;
RL GENE 117:209-217(1992).
RN [3]
RP PRELIMINARY SEQUENCE OF 27-62.
RM 91226375
RA KISHI J.I., OGAWA K., YAMAMOTO S., HAYAKAWA T.;
RL MATRIX 11:10-16(1991).
CC -1- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
CC AND IRREVERSIBLY INACTIVATE THEM.
CC -1- PTM: THE ACTIVITY OF TIMP-2 IS DEPENDENT ON THE PRESENCE OF
CC DISULFIDE BONDS.
CC -1- SIMILARITY: HIGH WITH OTHER MEMBERS OF THE TIMP FAMILY.
DR EMBL; X62622; MMTIMP2.
DR EMBL; M82858; MMTIMP2A.
DR EMBL; M93954; MMTIMP2B.
DR PIR; S15987; S15987.
DR PIR; JH0683; JH0683.

DR PROSITE; PS00288; TIMP.
KW METALLOPROTEASE INHIBITOR; SIGNAL.
FT SIGNAL 1 26
FT CHAIN 27 220
FT DISULFID 27 98
FT DISULFID 29 127
FT DISULFID 39 152
FT DISULFID 154 201
FT DISULFID 172 193
FT DISULFID 159 164
FT CONFLICT 12 12
FT CONFLICT 21 21
FT CONFLICT 195 195
FT CONFLICT 220 AA; 24328 MW; 244289 CN;
SQ SEQUENCE 220 AA; 24328 MW; 244289 CN;
DB 7; Score 1620; Match 97.3%; QryMatch 98.6%; Pred. No. 0.00e+00;
Matches 214; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
Db 1 mqaarslrlalglilllasivrpdadscspvhpqafcnadwvirkavsekevdsgnd 60
Qy 1 MGAARTLRALGLLLATLLRPADACSCSPVHPQAFCNADWVIRAKAVSEKEVDSGND 60
Db 61 iynpikriqveikqikmfkgpdieftyapssaavcgsldvsgkkeyliagkaegdg 120
Qy 61 IYGNPIKRIQVEIKQIKMFKGPEKDIEFTYAPSSAVCGSLDVSGKKEYLIAGKAEGDG 120
Db 121 kmhitlcdfivpwtltsitqkkslnhrygmgeckitrcpmpicyisspdeclwmdwvte 180
Qy 121 KMHITLCDFIVPWTLTSTQKKSINHRYQMGCEKITRCMPICYISSPDECLWMDWVTE 180
Db 181 ksnghqakffaciakrsdscawyrqaappkqefldiedp 220
Qy 181 KNINGHOAKFFACIKRSDGSCAWYRGAAPPKQEFLDIEDP 220
RESULT 3
ID TIM2 BOVIN STANDARD; PRT; 220 AA.
AC P16368;
DT 01-AUG-1990 (REL. 15, CREATED)
DT 01-MAY-1991 (REL. 18, LAST SEQUENCE UPDATE)
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE METALLOPROTEINASE INHIBITOR 2 PRECURSOR (TIMP-2) (TISSUE INHIBITOR OF
DE METALLOPROTEINASES-2) (COLLAGENASE INHIBITOR).
OS BOS TAURUS (BOVINE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; ARTIODACTYLA.
RN [1]
RP SEQUENCE FROM N.A.
RM 90207285
RA BOONE T.C., JOHNSON M.J., DE CLERCK Y.A., LANGLEY K.E.;
RL PROC. NATL. ACAD. SCI. U.S.A. 87:2800-2804 (1990).
RN [2]
RP SEQUENCE OF 27-71.
RC TISSUE=CARILAGE;
RM 86140235
RA MURRAY J.B., ALLISON K., SUDHALTER J., LANGER R.;
RL J. BIOL. CHEM. 261:4154-4159 (1986).
RN [3]
RP SEQUENCE OF 27-71.
RM 90008914

RA DE CLERCK Y.A., YEAN T.D., RATZKIN B.J., LU H.S., LANGLEY K.E.;
RL J. BIOL. CHEM. 264:17445-17453 (1989).
CC -!- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
CC -!- AND IRREVERSIBLY INACTIVATE THEM.
CC -!- PTM: THE ACTIVITY OF TIMP-2 IS DEPENDENT ON THE PRESENCE OF
CC -!- DISULFIDE BONDS.
CC -!- SIMILARITY: HIGH WITH OTHER MEMBERS OF THE TIMP FAMILY.
DR EMBL; M32303; BMMET.
DR PIR; A25322; A25322.
DR PIR; A35996; A35996.
DR PIR; A34468; A34468.
DR PROSITE; PS00288; TIMP.
KW METALLOPROTEASE INHIBITOR; SIGNAL.
FT SIGNAL 1 26
FT CHAIN 27 220
FT DISULFID 27 98
FT DISULFID 29 127
FT DISULFID 39 152
FT DISULFID 154 201
FT DISULFID 172 193
FT DISULFID 159 164
FT CONFLICT 56 56
FT CONFLICT 68 68
FT CONFLICT 220 AA; 24355 MW; 234318 CN;
SQ SEQUENCE 220 AA; 24355 MW; 234318 CN;
DB 7; Score 1550; Match 91.8%; QryMatch 94.3%; Pred. No. 0.00e+00;
Matches 202; Conservative 12; Mismatches 6; Indels 0; Gaps 0;
Db 1 mqaarslrlalglilllasivrpdadscspvhpqafcnadwvirkavsekevdsgnd 60
Qy 1 MGAARTLRALGLLLATLLRPADACSCSPVHPQAFCNADWVIRAKAVSEKEVDSGND 60
Db 61 iynpikriqveikqikmfkgpdieftyapssaavcgsldvsgkkeyliagkaegdg 120
Qy 61 IYGNPIKRIQVEIKQIKMFKGPEKDIEFTYAPSSAVCGSLDVSGKKEYLIAGKAEGDG 120
Db 121 nmhitlcdfivpwtltsatqkkslnhrygmgeckitrcpmpicyisspdeclwmdwvte 180
Qy 121 KMHITLCDFIVPWTLTSTQKKSINHRYQMGCEKITRCMPICYISSPDECLWMDWVTE 180
Db 181 ksnghqakffaciakrsdscawyrqaappkqefldiedp 220
Qy 181 KNINGHOAKFFACIKRSDGSCAWYRGAAPPKQEFLDIEDP 220
RESULT 4
ID TIM3 HUMAN STANDARD; PRT; 211 AA.
AC P35623;
DT 01-JUN-1994 (REL. 29, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE METALLOPROTEINASE INHIBITOR 3 PRECURSOR (TIMP-3) (TISSUE INHIBITOR OF
DE METALLOPROTEINASES-3).
GN TIMP3.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.

RC	TISSUE=KIDNEY;
RM	94215920
RA	SILBIGER S.M., JACOBSEN V.L., CUPPLES R.L., KOSKI R.A.;
RL	GENE 141:293-297(1994).
RL	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=BREAST CARCINOMA;
RM	94228524
RA	URIA J.A., FERRANDO A.A., VELASCO G., FREIJE J.M., LOPEZ-OTIN C.;
RL	CANCER RES. 54:2091-2094(1994).
RL	[3]
RN	SEQUENCE OF 14-211 FROM N.A.
RC	TISSUE=PLACENTA;
RM	94245184
RA	Apte S., MATTEI M., OLSEN B.;
RL	GENOMICS 19:186-90(1994).
CC	-!- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
CC	AND IRREVERSIBLY INACTIVATE THEM.
CC	-!- SIMILARITY: HIGH WITH OTHER MEMBERS OF THE TIMP FAMILY.
DR	EMBL; U02571; HS02571.
DR	EMBL; X76227; HSTIMP3.
DR	EMBL; L15078; HSTIMP3A.
DR	PIR; S45317; S45317.
DR	MIM; I88826; 11TH EDITION..
DR	PROSITE; PS00288; TIMP.
KW	METALLOPROTEINASE INHIBITOR; SIGNAL.
FT	POTENTIAL.
FT	CHAIN 1 22
FT	DISULFID 23 211 FT
FT	DISULFID 24 91
FT	BY SIMILARITY.
FT	DISULFID 26 118
FT	BY SIMILARITY.
FT	DISULFID 36 143
FT	BY SIMILARITY.
FT	DISULFID 145 192
FT	BY SIMILARITY.
FT	DISULFID 150 155
FT	BY SIMILARITY.
FT	DISULFID 163 184
FT	CONFLICT 21 22
FT	AE -> R (IN REF. 3).
SQ	SEQUENCE 211 AA; 24145 MW; 244095 CN;
DB	7; Score 695; Match 43.6%; OryMatch 42.3%; Pred. No. 8.10e-14
Matches	95; Conservative 56; Mismatches 55; Indels 12; Gaps 1
Db	2 tpwlgllvlgswlsgdgaeeactspshqpdafncsdsvirakvvgkklvkpgp--fgt 59
Qy	: : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy	7 TLRLALGLLLLA-TLL-RPADACSCLPVHPQQAFCNADVVIRAKAVSEKVDGNDIVGN 64
Db	60 -L--v-ytiqkmkyrgftkmbphvyihtheaseslcglklevn-kyqylltgrvy-dgkm 113
Qy	: : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy	65 PIKRITVEIKQIRMFKG-PEK-DIEFIYTPSSAVCGVLDVGKGKEYLIAGKAEGDKM 122
Db	114 yrgicnfvewdltlsqrkglnlyrhlgcnckikscyyipcfvtsekneclwtcdmlsnfg 173
Qy	: : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy	123 HTTIGDFIVPWDTLSTLTQRKSLSNHRYQGSCCKTRCPMTYISSDFDCLMDWDWTENK 182
Db	174 yptvgskhyacirqkgycswyrwgappdkksinatdp 211
Qy	: : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy	183 INGHOAKFFACIKRSDGSCAWYRGAAAPPKQFLDIEDP 220
RESULT	5
ID	TIM3 MOUSE
AC	P39876;
	STANDARD; PRT; 211 AA.

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DT      01-FEB-1995 (REL. 31, CREATED)
DT      01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT      01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE       METALLOPROTEINASE INHIBITOR 3 PRECURSOR (TIMP-3) (TISSUE INHIBITOR OF
GN        TIMP-3
OS MOS MUSCULUS (MOUSE).
OC EURAYOTIA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
ON BUTHERIA; RODENTIA.
[1]
RP     SEQUENCE FROM N.A.
RM    94179361
RA   LECO K.J., KHOKHA R., PAVLOFF N., HAWKES S.P., EDWARDS D.R.;
RL   J. BIOL. CHEM. 269:9352-9360 (1994).
RN [2]
RP     SEQUENCE FROM N.A.
RC STRAIN=BALE/C; TISSUE=SKIN, AND LUNG;
RM    94163596
RA   SUN Y., HEGAMYER G., COLBURN N.H.;
RL   CANCER RES. 54:1139-1144 (1994).
RN [3]
RP     SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA   OLSEN B.R.;
RN APTÉ S.-S., HAYASHI K., SELDIN M.F., MATTEI M.-G., HAYASHI M.,
RR SUBMITTED (XXX-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC -!- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCh AS COLLAGEenASES)
CC -!- SIMILARITY: HIGH WITH OTHER MEMBERS OF THE TIMP FAMILY.
DR EMBL; I27424; MMtIMP3X.
DR EMBl; Z30970; MMtIMP3MI.
DR EMBL; l19622; MMtIMP3A.
DR PIR; A53532; A53532.
DR PIR; s43052; s43052.
KW METALLOPRotease Inhibitor; SIGNAL.
FT      SIGNAL              1 22 POTENTIAL.
FT      CHAIN               23 211 METALLOPROteinAsE InhibITOR 3.
FT DISUlfID                24 91 BY SIMILARITy.
FT DISUlfID                 26 118 By SiMiLARiTy.
FT DISUlfID                  36 143 By SiMiLARiTy.
FT DISUlFId                145 192 By SiMiLARiTy.
FT DISUlFIld                150 155 By SiMiLARITy.
FT DISulfID                 163 184 By SiMiLARITy.
FT SEQUeNCE                 211 AA; 24182 MW; 246088 CN;
SQ
DB 7; Score         686; Match 43.1%; QryMatch 41.8%; Pred. No. 1.77e-142;
Matches          94; Conservative           56; Mismatches            56; Indels 12; Gaps 10;
Db      2 tpbwlgivllscwsighgwaeactcspshpqdafcnsdvirkavvggkklvkcp--fgt 59
QY      7 TURIALGLLLLA-TL-LRPA DACSCSFVEHQAFCAWVIVRAKA VSEKEVD SGNDIYN 64
Db      60 -l-v-ytiqmkmyrfgskmhpvyihtheasesicglklevn-kcyqllyltgrvy--egkm 113
QY      65 PIKRIOYEIKQIMFKG-P EK-DIEFIYTPAPSAVCVS LDVGGRKEYLIAAGAE GDGM 122
Db      114 ytglenfverwdhtlsqrkglnrvnyhlgncknikescyylpofvtcsknclwt dmlsnfg 173
QY      123 HTLCDFVPWDLTSTTKRSLSNHRYQMGECKITRPCMPICYISSPDEC LMDDWVTERN 182
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Db 174 ypqyqkvhacitqkgycswrgwappdkaisnatdp 211
 Qy 183 INGHQAKFFACIKRSDGSCAWIRGAAPPKQEFLDIEDP 220

RESULT 6
 ID TIM3 CHICK STANDARD; PRT; 212 AA.
 AC P26652;
 DT 01-AUG-1992 (REL. 23, CREATED)
 DT 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
 DE METALLOPROTEINASE INHIBITOR 3 PRECURSOR (TIMP-3) (TISSUE INHIBITOR OF
 DE METALLOPROTEINASES-3) (21 KD PROTEIN OF EXTRACELLULAR MATRIX).
 GN IMP-3.
 OS GALLUS GALLUS (CHICKEN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
 OC GALLIFORMES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=EMBRYO FIBROBLAST;
 RM 92381050
 RA PAVLOFF N., STASKUS P.W., KISHANANI N.S., HAWKES S.P.;
 RL J. BIOL. CHEM. 267:17321-17326(1992).
 RN [2]
 RP SEQUENCE OF 25-53.
 RC TISSUE=FIBROBLAST;
 RM 91093162
 RA STASKUS P.W., MASLARZ F.R., PALLANCK L.J., HAWKES S.P.;
 RL J. BIOL. CHEM. 266:449-454(1991).
 CC -1- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
 CC AND IRREVERSIBLY INACTIVATE THEM.
 CC -1- SIMILARITY: HIGH WITH OTHER MEMBERS OF THE TIMP FAMILY.
 DR ENBL; M94531; GGHTMP3A.
 DR PIR; A39043; A39043.
 DR PIR; A43429; A43429.
 DR PROSITE; PS00288; TIMP.
 KW METALLOPROTEINASE INHIBITOR; SIGNAL.
 FT SIGNAL 1 24
 FT CHAIN 25 212 METALLOPROTEINASE INHIBITOR 3.
 FT DISULFID 25 92 BY SIMILARITY.
 FT DISULFID 27 119 BY SIMILARITY.
 FT DISULFID 37 144 BY SIMILARITY.
 FT DISULFID 146 193 BY SIMILARITY.
 FT DISULFID 151 156 BY SIMILARITY.
 FT DISULFID 164 185 BY SIMILARITY.
 SQ SEQUENCE 212 AA; 24504 MW; 238212 CN;

DB 7; Score 686; Match 45.2%; QryMatch 41.8%; Pred. No. 1.77e-142;
 Matches 90; Conservative 49; Mismatches 50; Indels 10; Gaps 8;
 Db 22 aeactcvplhpqdfacnsdivirakvvgkImkdp--fgt-m-r--ytvqkmkmytqfq 75
 Qy 24 ADACSSPVPQAFQCNADVIRAKAVSEKVEVDSNDIYGNPKIRIQEIKQIKMFKG-P 82
 Db 76 imphvqviyteaseslcvqklevn-kyqyvitgrvy-egkvytglcnwyekwdrltIsqr 133
 Qy 83 EK-DIEFIYAPSSAVCGVSLDVGKKEYLIAGKAEQDKMHITLCDFIVPDWTLSTQK 141
 Db 134 kglnhryhlgcgckirpvyllpcfatckneclwtmnlfnghsgtqkhyacigrvegyc 193
 :|||||:| | | :|||:| | | :|||:| | | :|||:| | | :|||:| | | :|||:| | |

Qy 142 KSLNRYQMGECKITRCMPICVYISSPDECLMDWVTEKININGHOAKFFACIKRSDGSC 201
 Db 194 awyrgwappdktiinatdp 212
 Qy 202 AWYRGAAPPKQEFLDIEDP 220

RESULT 7
 ID TIM1 HUMAN STANDARD; PRT; 207 AA.
 AC P01033;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
 DE METALLOPROTEINASE INHIBITOR 1 PRECURSOR (TIMP-1) (ERYTHROID
 DE POTENTIATING ACTIVITY) (EPA) (TISSUE INHIBITOR OF METALLOPROTEINASES)
 DE (FIBROBLAST COLLAGENASE INHIBITOR) (COLLAGENASE INHIBITOR).
 GN TIMP1 OR TIMP.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RM 86040463
 RA DOCHERTY A.J.P., LYONS A., SMITH B.J., WRIGHT E.M., STEPHENS P.E.,
 RA HARRIS T.J.R., MURPHY G., REYNOLDS J.J.;
 RL NATURE 318:66-69(1985).
 RN [2]
 RP SEQUENCE FROM N.A.
 RM 85240567
 RA GASSON J.C., GOLDE D.W., KAUFMAN S.E., WESTBROOK C.A., HEWICK R.M.,
 RA KAUFMAN R.J., WONG G.G., TEMPLE P.A., LEARY A.C., BROWN E.L.,
 RA ORR E.C., CLARK S.C.;
 RL NATURE 315:768-771(1985).
 RN [3]
 RP SEQUENCE FROM N.A.
 RM 86205964
 RA CARMICHAEL D.F., SOMMER A., THOMPSON R.C., ANDERSON D.C., SMITH C.G.,
 RA WELGUS H.G., STRICKLIN G.P.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 83:2407-2411(1986).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA KACZOREK M., HONORE N., RIBES V., DEHOUX P., CORNET P., CARTWRIGHT T.,
 RA STREECK R.E.;
 RL BIO/TECHNOLOGY 5:595-598(1987).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=OVARY;
 RM 91025550
 RA RAPP G., FREUDENSTEIN J., KLAUDINY J., MUCHA J., WEMPE F., ZIMMER M.,
 RA SCHEIT K.H.;
 RL DNA CELL BIOL. 9:479-485(1990).
 RN [6]
 RP DISULFIDE BONDS, AND PARTIAL SEQUENCE.
 RM 90303199
 RA WILLIAMSON R.A., MARTSON F.A.O., ANGAL S., KOKLITIS P., PANICO M.,
 RA MORRIS H.R., CAENE A.F., SMITH B.J., HARRIS T.J.R., FREEDMAN R.B.;
 RL BIOCHEM. J. 268:267-274(1990).
 RN [7]
 RP SEQUENCE OF 24-38.
 RC TISSUE=SYNOVIAL FLUID;

[illegible]

RESULT	8
ID	TIMI RABIT STANDARD; PRT; 206 AA.
AC	P20614;
DT	01-FEB-1991 (REL. 17, CREATED)
DT	01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
DT	01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE	METALLOPROTEINASE INHIBITOR 1 PRECURSOR (TIMP-1).
OS	ORYCTOLAGUS CUNICULUS (RABBIT).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC	EUTHERIA; LAGOMORPHA.
RN	[1]
RP	SEQUENCE FROM N.A.
RM	89214135
RA	HOROWITZ S., DAFNI N., SHAPIRO D.L., HOLM B.A., NOTTER R.H.,
RA	QUIMBLE D.J.;
RL	J. BIOL. CHEM. 264:7092-7095(1989).
CC	-!- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES) AND IRREVERSIBLY INACTIVATE THEM.
CC	-!- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF DISULFIDE BONDS.
CC	-!- SIMILARITY: HIGH WITH OTHER MEMBERS OF THE TIMP FAMILY.
DR	EMBL; J04712; OSTIMP.
DR	FIR; A33350; A33350.
DR	PROSITE; F500288; TIMP.
KW	GLYCOPROTEIN; METALLOPROTEINASE INHIBITOR; ERYTHROCYTE MATURATION;
KW	SIGNAL.
FT	SIGNAL 1 23
FT	CHAIN 24 206
FT	DISULFID 24 93
FT	DISULFID 26 122 BY SIMILARITY.
FT	DISULFID 36 147 BY SIMILARITY.
FT	DISULFID 150 196 BY SIMILARITY.
FT	DISULFID 155 160 BY SIMILARITY.
FT	DISULFID 168 188 BY SIMILARITY.
FT	CARBOHYD 53 53 POTENTIAL.
FT	CARBOHYD 101 101 POTENTIAL.
SEQ	SEQUENCE 206 AA; 22758 MW; 218998 CN;
DB	7; Score 518; Match 40.1%; QryMatch 31.5%; Pred. No. 2.84e-99
Matches	79; Conservative 39; Mismatches 71; Indels 8; Gaps 8
D	b 7 laasmlilwlvparactcvpphqtafcnsdlvirakfvgaevnhntt-lydryeiakt 65 : : : : : : : :
Q	y 10 LAUGLLLATLLEPADACSCSPVHQFCADVIRAKAVSEKVDSGNDIYGN-PIKR 68 : : : : : : : :
D	b 66 tk-mfkfdgal-ghatdirfvytpameaygshksqrseefliagqlr-ngllhttc 122 : : : : : : : :
Q	y 69 IQVEIKQIKMFKEPKEDIEFIYTAPSAAVCVSLDVDGKKK-YLIAGKAEGDKMHITLC 127 : : : : : : : :
D	b 123 sfvvpwnslsfqrgsfktyaaogdmctvtfacapichlesdthclwtsslgsg-kgf 181 : : : : : : : :
Q	y 128 DFIVPDWTLSSTTKSLNHRYQMGE-CKITRCMPICYISSPECLMDWDVTEKNIGH 186 : : : : : : : :
D	b 182 qsrhlaclpqegplcaw 198 : :
Q	y 187 QAFFACIAKRSOGSCAW 203
RESULT	9

ID TIM1 BOVIN STANDARD; PRT; 207 AA.
AC P20414;
DT 01-FEB-1991 (REL. 17, CREATED)
DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
DT 01-FEB-1991 (REL. 25, LAST ANNOTATION UPDATE)
DE METALLOPROTEINASE INHIBITOR 1 PRECURSOR (TIMP-1).
OS BOS TAURUS (BOVINE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; ARTIODACTYLIA.
RN [1]
RN SEQUENCE FROM N.A.
RM 90365711
RA FREUDENSTEIN J., WAGNER S., LUCK R.M., EINSPIANIER R., SCHEIT K.H.;
RL BIOCHEM. BIOPHYS. RES. COMMUN. 171:250-256(1990).
RN [2]
RN PRELIMINARY SEQUENCE OF 24-69.
RA DE CLERCK Y.A., YEAN T.D., RATZKIN B.J., LU H.S., LANGLEY K.E.;
RL J. BIOL. CHEM. 264:17445-17453(1989).
CC -1- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
CC AND IRREVERSIBLY INACTIVATE THEM.
CC -1- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF
CC DISULFIDE BONDS.
CC -1- SIMILARITY: HIGH WITH OTHER MEMBERS OF THE TIMP FAMILY.
DR EMBL; M60073; BTMIM.
DR PIR; A35685; A35685.
DR PIR; B34468; B34468.
DR PROSITE; PS00288; TIMP.
KW GLYCOPROTEIN; METALLOPROTEINASE INHIBITOR; ERYTHROCYTE MATURATION;
KW SIGNAL.
FT SIGNAL 1 23
FT CHAIN 24 207 METALLOPROTEINASE INHIBITOR 1.
FT DISULFID 24 93 BY SIMILARITY.
FT DISULFID 26 122 BY SIMILARITY.
FT DISULFID 36 147 BY SIMILARITY.
FT DISULFID 150 197 BY SIMILARITY.
FT DISULFID 155 160 BY SIMILARITY.
FT DISULFID 168 189 BY SIMILARITY.
FT CARBOHYD 53 53 POTENTIAL.
FT CARBOHYD 101 101 POTENTIAL.
SQ SEQUENCE 207 AA; 23031 MW; 216327 CN;
DB 7; Score 517; Match 39.6%; QryMatch 31.5%; Pred. No. 5.09e-99;
Matches 78; Conservative 42; Mismatches 70; Indels 7; Gaps 7;
Db 7 maegilllllwtapactcypbqtafcnsdvirakfvgtaevne-talyqryeikm 65
Qy 10 LALGLLLLTLLRPADACSCSPVHPQQAFCNADVIRAKVSEKVDGNDIYGN-PIKR 68
Db 66 tk-mfkfgfealrdap-dirfiytpamevcgyfhrsqrseefliagql-snglhitc 122
Qy 69 IQVEIKQIKWFKGPEKIDIEFIYFAPSACVGVSLDVGCKE-YLIAGKAECDCKMHITC 127
Db 123 sfvapwnsmasqrrgftktyaaageectvfpcssipcklqsdthclwtddqlltgsckgf 182
Qy 128 DFIVPMDTLSTTKKSLNHRVQMGE-CKITRCMPICVSISSPDECLMDWVTEKINGH 186
Db 183 qsrhlacclprepglctw 199
Qy 187 QAKFACIKRSDGSCAW 203

RESULT 10
ID TIM1 MOUSE STANDARD; PRT; 205 AA.
AC P12032; P20064;
DT 01-OCT-1989 (REL. 12, CREATED)
DT 01-MAY-1991 (REL. 18, LAST SEQUENCE UPDATE)
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE METALLOPROTEINASE INHIBITOR 1 PRECURSOR (TIMP-1) (ERYTHROID
DE POTENTIATING ACTIVITY) (EPA) (TISSUE INHIBITOR OF METALLOPROTEINASES)
DE (COLLAGENASE INHIBITOR 1608 FIBROBLAST) (TPA-INDUCED PROTEIN)
DE (TPA-S1).
GN TIMP-1.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RN SEQUENCE FROM N.A.
RM 87218524
RA GEWERT D.R., COULOMBE B., CASTELINO M., SKUP D., WILLIAMS B.R.G.;
RL EMBO J. 6:651-657(1987).
RN [2]
RN SEQUENCE FROM N.A.
RC TISSUE=FIBROBLAST;
RM 87066763
RA EDWARDS D.R., WATERHOUSE P., HOLMAN M.L., DENHARDT D.T.;
RL NUCLEIC ACIDS RES. 14:8863-8878(1986).
RN [3]
RN SEQUENCE FROM N.A.
RC STRAIN=C3H;
RM 88038821
RA JOHNSON M.D., HOUSEY G.M., KIRSCHMEIER P.T., WEINSTEIN I.B.;
RL MOL. CELL. BIOL. 7:2821-2829(1987).
CC -1- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
CC AND IRREVERSIBLY INACTIVATE THEM.
CC -1- FUNCTION: ALSO MEDIATES ERYTHROPOIESIS IN VITRO; BUT, UNLIKE IL-3,
CC IT IS SPECIES-SPECIFIC, STIMULATING THE GROWTH AND DIFFERENTIATION
CC OF ONLY HUMAN AND MURINE ERYTHROID PROGENITORS.
CC -1- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF
CC DISULFIDE BONDS.
CC -1- INDUCTION: BY VIRUS.
CC -1- INDUCTION: REGULATED BY TUMOR PROMOTERS AND MITOGENS THROUGH
CC PROTEIN KINASE C.
CC -1- SIMILARITY: HIGH WITH OTHER MEMBERS OF THE TIMP FAMILY.
DR EMBL; M28308; MMEPAMP1.
DR EMBL; X04684; MM16C8.
DR EMBL; M17243; MMTPAS1.
DR PIR; A26633; A26633.
DR PIR; A26106; A26106.
DR PIR; A26917; A26917.
DR PROSITE; PS00288; TIMP.
KW GLYCOPROTEIN; METALLOPROTEINASE INHIBITOR; ERYTHROCYTE MATURATION;
KW SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 205 METALLOPROTEINASE INHIBITOR 1.
FT DISULFID 25 94 BY SIMILARITY.
FT DISULFID 27 123 BY SIMILARITY.
FT DISULFID 37 148 BY SIMILARITY.
FT DISULFID 151 197 BY SIMILARITY.
FT DISULFID 156 161 BY SIMILARITY.

FT	DISULFID	169	189	BY SIMILARITY.
FT	CARBOHYD	54	54	POTENTIAL.
FT	CARBOHYD	102	102	POTENTIAL.
FT	CONFLICT	52	52	E -> R (IN REF. 1).
FT	CONFLICT	66	66	M -> MM (IN REF. 1).
FT	CONFLICT	117	118	NL -> KF (IN REF. 1).
FT	CONFLICT	121	121	S -> N (IN REF. 1).
FT	CONFLICT	139	139	A -> V (IN REF. 1).
FT	CONFLICT	143	143	T -> KN (IN REF. 1).
FT	CONFLICT	194	194	P -> L (IN REF. 1).
SSQ	SEQUENCE	205 AA; 22628 MW; 216139 CN;		
DB	7; Score	506; Match 38.6%; QryMatch 30.8%; Pred. No. 3.16e-96;		
	Matches	76; Conservative 43; Mismatches 70; Indels 8; Gaps 8;		
dbb	8	laagilllllalllaakacacappbqtaafcnsldivrakfmgapeinett-lyqrvyklkm 66		
Qy	10	LAUGILLALLTLIRPADACSPVHPQQAFQADVVIRAKAVSEKVDGNDIYGN-PIKR 68		
dbb	67	tk-mlkgfkav-gnaadirayatpymeslcygahkxsnqrseeflitgrl-nqnhihsac 123		
Qy	69	IQVEIKQIKMFKGPEKDEIFYTAPSSAVGVSLDVGGKE-YLIAGKAEGDGKMHITLC 127		
dbb	124	sflvpwrtlspaqqrakfkytsagcgvctvfpcisipoklesdthclwtddvqlvs-edy 182		
Qy	128	DFIVPMDTLSTTKQSLNHRHYQMGCE-CKITRCFMPICYIISPPDECLWMDWTEKRNINH 186		
dbb	183	qsrhfacflprnpglctw 199		
Qy	187	QAKFFACIKRSDGSCAW 203		

RESULT	11	STANDARD;	PRT;	207 AA.
AD	TIMI PIG			
DC	P35624;			
DD	01-JUN-1994 (REL. 29, CREATED)			
DT	01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)			
DT	01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)			
DT	01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)			
DE	METALLOPROTEINASE INHIBITOR 1 PRECURSOR (TIMP-1).			
DE	SUS SCROFA (PIG).			
DE	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
DC	EUTHERIA; ARTIODACTYLA.			
CC	{1}			
CC	SEQUENCE FROM N.A.			
CC	TISSUE=OVARY;			
CC	92201478			
CC	TANAKA T., ANDOH N., TAKEYA T., SATO E.;			
CC	MOL. CELL. ENDOCRINOL. 83:65-71(1992).			
CC	-1- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)			
CC	AND IRREVERSIBLY INACTIVATE THEM.			
CC	-1- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF			
CC	DISULFIDE BONDS.			
CC	-1- SIMILARITY: HIGH WITH OTHER MEMBERS OF THE TIMP FAMILY.			
CC	EMBL; S96211; S96211.			
DR	PROSITE; PS00288; TIMP.			
DR	GLYCOPROTEIN; METALLOPROTEASE INHIBITOR; ERYTHROCYTE MATURATION;			
KW	SIGNAL.			
KW	SIGNAL.			
TT	1	23	BY SIMILARITY..	
TT	CHAIN	24	207	METALLOPROTEINASE INHIBITOR 1.
TT	DISULFID	24	93	BY SIMILARITY.

	FT	DISULFID	26	122	BY SIMILARITY.
	FT	DISOLFID	36	147	BY SIMILARITY.
	FT	DISOLFID	150	197	BY SIMILARITY.
	FT	DISOLFID	155	160	BY SIMILARITY.
	FT	DISOLFID	168	189	BY SIMILARITY.
	FT	CARBOHYD	53	53	POTENTIAL.
	FT	CARBOHYD	101	101	POTENTIAL.
	SQ	SEQUENCE	207 AA;	23098 MW; 218921 CN;	
	DB	7; Score	491; Match 39.6%; QryMatch 29.9%; Pred. No. 1.99e-92;		
	Matches	78; Conservative	37; Mismatches 75; Indels 7; Gaps 7;		
	Db	7 lasglllwtasractcvcphprtafccsadlvirakfvgapefnqtas-vqryeikm	65		
	QY	10 lALGILLLATLLRPACSCSPVHPQQAFCNADVVIRAKSEKEVGNDIYN-PKRR	68		
	Db	66 tk-mfkgnal-gdapdirfiyepamesvgyfrhsqrnsqefliaagql-wnghlhttc	122		
	QY	69 IQYEIKLIKMFKGPEKDIEFIYTAPSSAVCGVSLDVGCK-KEYLIAGKAEGDGGMHTLC	127		
	Db	123 sfvapwnslsaadrgtfeiyaageectvfcpctapioklsdthclwtdqllltgsedkgf	182		
	QY	128 DFIVPMDTLSTOKKSINHRYQMGE-CKITRCPIPCYSPPDECLMWDWVTETKNIGH	186		
	Db	183 gsrhlacmprepgmtcw	199		
	QY	187 OAKEFFACKRSDGS CA W	203		
	RESULT	12			
ID	TIMZ	RAT	STANDARD;	PRT:	22 AA.

RESULT	12
ID	TIMP-2 RAT
PRT;	STANDARD; PRT; 22 AA.
AC	P30121;
DT	01-APR-1993 (REL. 25, CREATED)
DDT	01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DDT	01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE	METALLOPROTEINASE INHIBITOR 2 (TIMP-2) (TISSUE INHIBITOR OF METALLOPROTEINASES - (FRAGMENT).
GN	TIMP-2.
OS	RATTUS NORVEGICUS (RAT).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC	EUTHERIA; RODENTIA.
[1]	
RP	SEQUENCE.
RM	92117648
RA	ROSWIT W.T., MCCOURT D.W., PARTRIDGE N.C., JEFFREY J.J.;
RR	ARCH. BIOCHEM. BIOPHYS. 292:402-410(1992).
CCC	- - FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES) AND IRREVERSIBLY INACTIVATE THEM.
CC	- - PTM: THE ACTIVITY OF TIMP-2 IS DEPENDENT ON THE PRESENCE OF DISULFIDE BONDS.
CC	- - SIMILARITY: HIGH WITH OTHER MEMBERS OF THE TIMP FAMILY.
CC	PIR; S20325; S20325.
DR	DR PROSITE; PS00288; TIMP.
KW	METALLOPROTEASE INHIBITOR.
FT	NON TER 22 22
SQ	SEQUENCE 22 AA; 2374 MW; 2188 CN;

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DB 7; Score 164; Match 100.0%; QryMatch 10.0%; Pred. No. 9.30e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 cscspvhqgafcnadvirak 22
 QY 27 CSCSPVHPQAFCNADVIRAK 48

RESULT 13
 ID T1M1 RAT STANDARD; PRT; 22 AA.
 AC P30120;
 DT 01-APR-1993 (REL. 25, CREATED)
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
 DE METALLOPROTEINASE INHIBITOR 1 (TIMP-1) (FRAGMENT).
 GN TIMP-1.
 OS RATTUS NORVEGICUS (RAT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE.
 RM 92117648
 RA ROSWIT W.T., MCCOURT D.W., PARTRIDGE N.C., JEFFREY J.J.;
 RL ARCH. BIOCHEM. BIOPHYS. 292:402-410(1992).
 CC -1- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
 CC AND IRREVERSIBLY INACTIVATE THEM.
 CC -1- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF
 CC DISULFIDE BONDS.
 CC -1- SIMILARITY: HIGH WITH OTHER MEMBERS OF THE TIMP FAMILY.
 DR PIR; S20326; S20326.
 DR PROSITE; PS00288; TIMP.
 KW METALLOPROTEASE INHIBITOR.
 FT NON TER 22 22
 SQ SEQUENCE 22 AA; 2363 MW; 2292 CN;

DB 7; Score 136; Match 77.3%; QryMatch 8.4%; Pred. No. 1.43e-09;
 Matches 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 1 cscapthpqtafcnadvirak 22
 QY 27 CSCSPVHPQAFCNADVIRAK 48

RESULT 14
 ID HYPB-ECOLI STANDARD; PRT; 290 AA.
 AC P24190;
 DT 01-MAR-1992 (REL. 21, CREATED)
 DT 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
 DE HYDROGENASE ISOENZYMES FORMATION PROTEIN HYPB.
 GN HYPB.
 OS ESCHERICHIA COLI.
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
 OC ENTEROBACTERIACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RM 91194542
 RA LUTZ S., JACOBI A., SCHLENSOG V., BOEHM R., SAVERS G., BOECK A.;
 RL MOL. MICROBIOL. 5:123-135(1991).
 CC -1- FUNCTION: IS REQUIRED FOR THE FORMATION OF ALL THREE HYDROGENASE
 CC ISOENZYMES. AFFECTS SOME ASPECT OF THE PROCESSING OF HYDROGENASES
 CC 1 AND 2, PERHAPS NICKEL INCORPORATION INTO THE APO-ENZYMES, SINCE
 CC HYPB GENE LESIONS CAN BE COMPLEMENTED BY HIGH NICKEL ION

CC CONCENTRATION IN THE MEDIUM.
 CC -1- SIMILARITY: BELONGS TO THE HYPB/HOPM FAMILY.
 DR EMBL; X54543; ECHYP.
 DR PIR; S15198; S15198.
 DR ECO2DBASE; E031.0; 6TH EDITION.
 DR ECOGENE; E010484; HYPB.
 KW NICKEL.
 SQ SEQUENCE 290 AA; 31624 MW; 398662 CN;

DB 4; Score 117; Match 25.2%; QryMatch 7.1%; Pred. No. 1.13e-05;
 Matches 27; Conservative 27; Mismatches 48; Indels 5; Gaps 5;

Db 120 lltetlmrlkdvpcavieqgqvtvndaarirattgttgaigvntgkghida-qmia-daa 177
 QY 15 LLLATLLRPADACSCSPVHPQAFCNADVIRAKVSEKVDGNDIYGNPIKRIQYEIK 74

Db 178 p-rl-plddngilfi-envgnlvcpsafldlgekhkavlavtegedk 221
 QY 75 QIKMFKEKDIEFIYITAPSSAVCGVSLDVGKKEYLIAGKAGDGK 121

RESULT 15
 ID YB07 YEAST STANDARD; PRT; 1025 AA.
 AC P38065;
 DT 01-OCT-1994 (REL. 30, CREATED)
 DT 01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
 DE ALPHA-ADAPTIN HOMOLOG IN URA7-POL12 INTERGENIC REGION.
 GN YBLO37W OR YBLO412.
 OS SACHAROMYCES CEREVISIAE (BAKER'S YEAST).
 OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C;
 RA DE WERGIFOSSE P., JACQUES B., JONNIAUX J.L., PURNELLE B., SKALA J.,
 RA GOFFEAU A.;
 RL YEAST 10:1489-1496(1994).
 CC -1- SIMILARITY: STRONG, TO ALPHA ADAPTINS.
 DR EMBL; X78214; SC22KBF.
 DR PIR; S42507; S42507.
 KW HYPOTHETICAL PROTEIN; COATED PITS.
 SQ SEQUENCE 1025 AA; 115011 MW; 5722309 CN;

DB 8; Score 98; Match 29.5%; QryMatch 6.0%; Pred. No. 1.85e-02;
 Matches 23; Conservative 16; Mismatches 34; Indels 5; Gaps 4;

Db 842 phkraeqyevsirkpfavedspilalhfkcggtetnlnktaigmttttis--sdvnps 899
 QY 65 PIKRI-Q-YELIKIMFGPEKDIEFIYITAPSSAVCGVSLDVG-GKKEYLIAGKAGDGK 121

Db 900 mhlmlaqfiskwktlsda 917
 QY 122 MHITLCLDFIVFWDTLSIT 139

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